



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 174903

TO: Manjunath N Rao
Location: rem/3B81/3C70
Art Unit: 1652
Tuesday, January 03, 2006
Case Serial Number: 09/990874

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

mg

174903

STIC-Biotech/ChemLib

From: Rao, Manjunath N.
Sent: Thursday, December 22, 2005 10:59 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request for 09990874

From: Manjunath N. Rao
Art Unit 1652, Room 3B81
Mail Box in Room 3C70
Phone: 272-0939

RECEIVED
DEC 22 AM
STIC

Date: 12-22-05

Please search the following as soon as possible for application with serial number

09/990,874

1. **SEQ ID NO: 55** against all commercial nucleic acid databases, issued patents/published applications database and pending application database.

Please provide a print of all results

If you have any questions please call me at the above phone number.

Thanks

12/22/2005

GenCore version 5.1.6
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OM protein - nucleic search, using frame plus pon model

Run on: December 30, 2005, 00:04:36 ; Search time 3238 Seconds
(without alignments)
3335.471 Million cell updates/sec

Title: US-09-990-874B-55

Perfect score: 1046
Sequence: 1 QTIQPGTGYDGYFYGYMND.....YQIVAVEGYFSGSASITVS 190

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlp
-Q=/cgn2_1/USFT0.spool_p/US09990874/runat_29122005_095048_5081/app_query.fasta_1.327
-DB=GenEmbl -QFMT=fastp -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09990874 @CGN 1 1 7415 @runat_29122005_095048_5081 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCKS=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.in.*
- 3: gb.env.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.sy.*
- 12: gb.un.*
- 13: gb.vi.*
- 14: gb.htg.*
- 15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	93.1	596	6	AX382226 Sequence
2	974	93.1	596	6	AX797706 Sequence
3	962	92.0	786	15	U24191 Trichoderma

4	948	90.6	573	6	AR031735 Sequence
5	946	90.4	1015	6	AR055687 Sequence
6	946	90.4	1020	15	TRXN1GNA
7	946	90.4	1075	15	S67387
8	870	83.2	672	15	AY320048 Trichoder
9	841	80.4	786	15	AY370020 Trichoder
10	840	80.3	841	15	AY156910 Trichoder
11	834	79.7	928	15	AY1012718 Trichoder
12	723	69.1	2208	15	NCB8B2
13	700	66.9	154038	15	NCB8G12
14	687	65.7	1281	6	AR149835 Sequence
15	687	65.7	1281	6	CQ847410 Sequence
16	687	65.7	1281	6	AR410556 Sequence
17	687	65.7	1281	15	CTH508931
18	680.5	65.1	863	15	AY366479
19	667.5	63.8	949	15	AJ863566
20	658.5	63.0	687	15	AY575961
21	656.5	62.8	1623	15	APB14BYL
22	654	62.5	1409	15	ANIDXYLA
23	649	62.0	1921	15	AY144350
24	645.5	61.7	89019	15	AX842624
25	644	61.6	2102	15	AB044941
26	643.5	61.5	588	6	AX244978
27	643.5	61.5	983	6	AR044575
28	643.5	61.5	983	6	AR157660
29	641.5	61.3	678	15	AY536639
30	641.5	61.3	816	15	AF490982
31	641.5	61.3	843	15	AY551187
32	641.5	61.3	2445	1	AB063255
33	640.5	61.2	851	6	A62443
34	639	61.1	1362	15	ANIDXYLB
35	638.5	61.0	2196	1	U01242
36	638.5	61.0	3204	1	AY795559
37	638.5	61.0	110000	1	CP000088_14
38	635.5	60.8	1889	15	ASXNYNE
39	635	60.7	1174	6	AR149836
40	635	60.7	1174	6	CQ847412
41	635	60.7	1174	6	AR410557
42	635	60.7	1174	15	CTH508932
43	633.5	60.6	695	15	CNS01CPS
44	633	60.5	1204	15	AF301904
45	633	60.5	1204	15	AF301905

ALIGNMENTS

RESULT 1	AX382226	AX382226	Sequence 39 from Patent WO0192487.	596 bp	DNA	linear	PAT 18-MAR-2002
LOCUS	AX382226	AX382226	Sequence 39 from Patent WO0192487.				
DEFINITION	AX382226	AX382226	Sequence 39 from Patent WO0192487.				
ACCESSION	AX382226	AX382226	Sequence 39 from Patent WO0192487.				
VERSION	AX382226.1	GI:19577009					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							

Sung W.L.
Modified xylanases exhibiting increased thermophilicity and alkalophilicity
Patent: WO 0192487-A 39 06-DEC-2001;
NATIONAL RESEARCH COUNCIL OF CANADA (CA)
Location/Qualifiers
1. .596
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="TrX"

ORIGIN

Alignment Scores:	1.17e-78	Length:	596
Pred. No.:	974.00	Matches:	179
Score:			

Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x AX382226 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
 DB 23 CAACAATATACACAGGACCGGTTACAAACACCGGTTACTTTTACAGCTATTGGAACGAT 82

QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyTyrGlnPheSerValAsnTyrSer 40
 DB 83 GGCCATGGTGGTGTACTTATACAAACCGGCGCCGAGGCCAATTTAGCGTCAATTTGGTCT 142

QY 41 AsnSerGlyAsnPheValGlyGlyGlyTyrGlnProGlyThrLysAsnLysValle 60
 DB 143 AACTCCGGAAACTTCGTAGGTGGAAAGGTTGGCAACCCGGGACCAAAAATAAGGTGATC 202

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSer 80
 DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATACCTTAAGCGTCTATGGCTGGTCT 262

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 263 AGAAACCCACTGATTGTAATATTCATATGTCGAAATTTCCGTACTACATCCGAGTACC 322

QY 101 GlyAlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 323 GGCGCCACAAAATTAGCGGAAGTCACTAGTATGGATCCGATATGATATCTACCGTACC 382

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerVal 140
 DB 383 CAACGCGTTAATCAGCCATCGATCATTTGGAAACCGCCACCTTTTATCAGTACTGGAGTGT 442

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAla 160
 DB 443 AGAGTAAATCATCGAGCTCCGTTCCGTTAATCTCGAATCACTTTAATGCAATGGCA 502

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 503 CAGCAAGGTTTAACTTACCTAGGTACAAATGATGATATCAATCGTAGCGGTGGAAGGCTACTTC 562

QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 563 TCGAGTGGTTCCTCGTAGTATTACAGTGAGC 592

RESULT 2
 AX797706 AX797706 596 bp DNA linear PAT 04-OCT-2003
 LOCUS
 DEFINITION Sequence 39 from Patent WO03046169.
 ACCESSION AX797706
 VERSION AX797706.1 GI:37518114
 KEYWORDS
 SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
 ORGANISM Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
 1 Sung, W. L.
 Xylanases with enhanced thermophilicity and alkalophilicity
 Patent: WO 03046169-A 39 05-JUN-2003;
 National Research Council of Canada (CA)
 Location/Qualifiers
 1. 596
 /organism="Hypocrea jecorina"
 /mol_type="unassigned DNA"
 /db_xref="taxon:51453"
 /note="xylanase"
 synthesized Trx sequence produced using synthetic
 oligonucleotide (SEQ ID Nos.21-38) as depicted in Figure
 2"

ORIGIN

Alignment Scores:
 Pred. No.: 1,17e-78 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x AX797706 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
 DB 23 CAACAATATACACAGGACCGGTTACAAACACCGGTTACTTTTACAGCTATTGGAACGAT 82

QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyTyrGlnPheSerValAsnTyrSer 40
 DB 83 GGCCATGGTGGTGTACTTATACAAACCGGCGCCGAGGCCAATTTAGCGTCAATTTGGTCT 142

QY 41 AsnSerGlyAsnPheValGlyGlyGlyTyrGlnProGlyThrLysAsnLysValle 60
 DB 143 AACTCCGGAAACTTCGTAGGTGGAAAGGTTGGCAACCCGGGACCAAAAATAAGGTGATC 202

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSer 80
 DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATACCTTAAGCGTCTATGGCTGGTCT 262

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 263 AGAAACCCACTGATTGTAATATTCATATGTCGAAATTTCCGTACTACATCCGAGTACC 322

QY 101 GlyAlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 323 GGCGCCACAAAATTAGCGGAAGTCACTAGTATGGATCCGATATGATATCTACCGTACC 382

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerVal 140
 DB 383 CAACGCGTTAATCAGCCATCGATCATTTGGAAACCGCCACCTTTTATCAGTACTGGAGTGT 442

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAla 160
 DB 443 AGAGTAAATCATCGAGCTCCGTTCCGTTAATCTCGAATCACTTTAATGCAATGGCA 502

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 503 CAGCAAGGTTTAACTTACCTAGGTACAAATGATGATATCAATCGTAGCGGTGGAAGGCTACTTC 562

QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 563 TCGAGTGGTTCCTCGTAGTATTACAGTGAGC 592

RESULT 3
 TRU24191 786 bp mRNA linear PLN 25-MAR-1997
 LOCUS
 DEFINITION Trichoderma reesei beta-xylanase (XYN2) mRNA, complete cds.
 ACCESSION U24191
 VERSION U24191.1 GI:780815
 KEYWORDS
 SOURCE Hypocrea jecorina
 ORGANISM Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 1 (bases 1 to 786)
 la Grange, D.C., Pretorius, I.S. and van Zyl, W. H.
 Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
 Saccharomyces cerevisiae
 Appl. Environ. Microbiol. 62 (3), 1036-1044 (1996)
 8975597
 2 (bases 1 to 786)
 van Zyl, W.
 Direct Submission
 Submitted (06-APR-1995) Willem H. van Zyl, University of
 Stellenbosch, Microbiology, Victoria street, Stellenbosch, 7600,


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FEATURES             South Africa
source               1. .786
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gene                1. .786
                    /gene="XYN2"
                    /note="endo-beta-1,4-xylanase; endoxylanase"
CDS                 /codon_start=1
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                    /protein_id="AAB50278.1"
                    /db_xref="GI:780816"
                    /translation="MVSPSTSLAGVAALISGLVAAPAEVEPVAVEKQTLPQGTGVNN
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SITVS"
sig_peptide         105..203
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mat_peptide         204..773
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                    /product="beta-xylanase"

ORIGIN
Alignment Scores:
Pred. No.:          1.92e-77      Length:      786
Score:              962.00        Matches:    177
Percent Similarity: 95.79%       Conservative: 5
Best Local Similarity: 93.16%    Mismatches: 8
Query Match:        91.97%       Indels:     0
DB:                 15           Gaps:       0

US-09-990-874B-55 (1-190) x TRU24191 (1-786)
QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
DB 204 CAGACGNTTCAGCCGCGACGGGTACACACGCGTACTTCCACTCGTACTGGACGAT 263
QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40
DB 264 GGCACGCGCGGTGACGTACACCAATGGTCCCGCGCGGAGTCTCCGTCAACTGGTCC 323
QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlyTyrGlnProGlyThrIleAsnValIle 60
DB 324 AACTCGGGCAACTTTGTTCGGCGGCAAGGGATGGCAGCCCGCACCAAGAACAGGTGATC 383
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrIleValIleValTyrGlyTyrSer 80
DB 384 AACTTCGGGCGAGTACACACCCACGCGACAGCTACTCTCCGTGTAGCGGTGGTCC 443
QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 444 CGCAACCCCTGATCGAGTACTACATCGTCGGGAACCTTGGCACCTACACCCGTCACG 503
QY 101 GlyAlaThrIleHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 504 GGGCGCCACCAAGCTGGGCGAGGTCACTCCGACGCGCAGCGCTACGACATTTACCGCAGC 563
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerVal 140
DB 564 CACGGGTCAACGACCGCTCATCATCGGCACCGCCACCTTTTACCAAGTACTGGTCCGTC 623
QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAla 160
DB 624 CGCCGCAACCAACCGCTCGAGCGGTCTCGTCAACACGCGCGAACCACCTTCAACGCGGTGGCT 683
QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
DB 684 CAGCAAGGCGCTGCGTCCGGACGATGATACAGATTGTCGCGTGGAGGGTACTTTT 743

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QY 181 SerSerGlySerAlaSerIleThrValSer 190
DB 744 AGCTCTGGCTCTGCTTCCATCACCGTCAGC 773

RESULT 4
AR031735
LOCUS
DEFINITION
AR031735
ACCESSION
AR031735.1 GI:5946024
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 573)
AUTHORS
Sung W.L., Yaguchi M. and Iehikawa K.
TITLE
Modification of xylanase to improve thermophilicity, alkophilicity
and thermostability
JOURNAL
Patent: US 5866408-A 18 02-FEB-1999;
FEATURES
Location/Qualifiers
1..573
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:          2.45e-76      Length:      573
Score:              948.00        Matches:    174
Percent Similarity: 95.24%       Conservative: 6
Best Local Similarity: 92.06%    Mismatches: 9
Query Match:        90.63%       Indels:     0
DB:                 6           Gaps:       0

US-09-990-874B-55 (1-190) x AR031735 (1-573)
QY 2 ThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAspGly 21
DB 3 AGCATAGGACCGAAACCGGTTTCAACACCGTTACTTTTACAGCTATTTCGACGATGGC 62
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSerAsn 41
DB 63 CATGGTGGTGTATACCTATACAAACGGGCGCGGACCAATTTAGCGCTCAATTTGGTCTAAC 122
QY 42 SerGlyAsnPheValGlyGlyGlyTyrGlnProGlyThrIleAsnValIleAsn 61
DB 123 TCCGGAAACTTCGTAGTGGAAAGGTGGCAACCGGGACCAANAATAAGGTGATCAAC 182
QY 62 PheSerGlySerTyrAsnProAsnGlyAsnSerTyrIleAlaValTyrGlyTyrSerArg 81
DB 183 TTCTCTGGATCTTATAATCGAATGGGAATTCATCTTAAGCGTCTATGCTGTCTAGA 242
QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGly 101
DB 243 AACCCACTGATTGAATATTACATTGTGAAATAATTCGGTACCTACCAATCCGAGTACCGGC 302
QY 102 AlaThrIleHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGln 121
DB 303 GCCACAAATTAGCGGAGTCACTAGTATGGATCGGTATATATATATCTACCGTACCCAA 362
QY 122 ArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArg 141
DB 363 CGGGTTAATCAGCCATCGATCATTTGGAACCGGCACCTTTTATCAGTACTGGAGTGTAGA 422
QY 142 ArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArg 161
DB 423 CGTACGCAATCGGAGCTCCGGTTCGGTTAATACGTGCAATCACCATTATGATGCGGCACAG 482
QY 162 GlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSer 181
DB 483 CAAAGGGTTAACCCCTAGGTACAATGGATTTCAATCTAGCGGTGGAGGCTACTTCTCG 542
QY 182 SerGlySerAlaSerIleThrValSer 190

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543 AGTGGTTCGGCTAGTATTACAGTGAGC 569
|||||
Db
RESULT 5
AR055687
LOCUS AR055687 1015 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5837515.
ACCESSION AR055687
VERSION AR055687.1 GI:5981264
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1015)
AUTHORS Suominen,P., Nevalainen,H., Saarelainen,R., Paloheimo,M. and
Fagerstrom,R.
TITLE Enzyme preparations and methods for their production
JOURNAL Patent: US 5837515-A 1 17-NOV-1998;
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 7,06e-76 Length: 1015
Score: 946.00 Matches: 179
Percent Similarity: 80.97% Conservative: 4
Best Local Similarity: 79.20% Mismatches: 7
Query Match: 90.44% Indels: 36
DB: 6 Gaps: 1
US-09-990-874B-55 (1-190) x AR055687 (1-1015)
Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTripanNap 20
Db 275 CAGACGATTTCAGCCGCGCACGGCTTACAAACACGGCTACTTCTACTCGTACTGGAACGAT 334
Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTripan 40
Db 335 GGCCACGGCGCGTACGTACCAATGGTCCCGCGCGCGAGTTCCTCGTCACTGGTCC 394
Qy 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLys ----- 58
Db 395 AACTCGGCAACTTGTTCGGCGCAAGGATGGCAGCCCGGACCAAGAACAGTAAGAC 454
Qy 58 ----- 58
Db 455 TACCTACTCTTACCCCTTTGACCAACACAGCACAAACATACAAACATGTGACTACC 514
Qy 59 -----ValIleAsnPheSerGly 64
Db 515 AATCATGGAATCGGATCTAACACAGCTGTGTTTAAATAAAGGGTCACTCACTTCGCGGA 574
Qy 65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeu 84
Db 575 AGCTACAACCCCAACCGGCAACAGTACTCTCCGCTAGCGGTGTCGCGCAACCCCTG 634
Qy 85 IleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLys 104
Db 635 ATCCAGTACTACATCGTCGAGAACCTTGGCACCCTACACCCCGTCCACGGGGCCACCAAG 694
Qy 105 HisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsn 124
Db 695 CTGGCGAGGTCACCTCCGACGCGCGCTCTACGACATTTACCGCACCGCGCGCTCAAC 754
Qy 125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgArgAsnArg 144
Db 755 CAGCCGTCATCATCGGCACCGCCACCTTTTACCAAGTACTGTGCTCGCGCGCACACAC 814
Qy 145 ArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTripanNap 164
Db 815 CGCTCAGCGGCTCCGTCAACACGCGGAACCACTTCAACGCGGTGGCTCAGCAAGGCTG 874

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165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
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875 ACGCTCGGACGATGGATTACCAAGTTGTCGCGTGGAGGGTACTTATAGCTCTGGCTCT 934
|||||
Qy 185 AlaSerIleThrValSer 190
Db 935 GCTTCCATCACCGTCAGC 952
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RESULT 6
TRXYNIGNA
LOCUS T.reesei xynl gene, complete CDS.
DEFINITION X69573 S51973
ACCESSION X69573.1 GI:396563
VERSION X69573.1
KEYWORDS xyl1 gene; xylanase.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
REFERENCE 1 (bases 1 to 1020)
AUTHORS Torronen,A., Mach,R.L., Messner,R., Gonzalez,R., Kalkkinen,N.,
Harkki,A. and Kubicek,C.P.
TITLE The two major xylanases from Trichoderma reesei: characterization
of both enzymes and genes
JOURNAL Biotechnology (N.Y.) 10 (11), 1461-1465 (1992)
FEATURES
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1..1020
Location/Qualifiers
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/mol_type="genomic DNA"
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intron
exon
ORIGIN
Alignment Scores:
Pred. No.: 7,1e-76 Length: 1020
Score: 946.00 Matches: 179
Percent Similarity: 80.97% Conservative: 4
Best Local Similarity: 79.20% Mismatches: 7
Query Match: 90.44% Indels: 36
DB: 15 Gaps: 1
US-09-990-874B-55 (1-190) x TRXYNIGNA (1-1020)
Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTripanNap 20
Db 295 CAGACGATTTCAGCCGCGCACGGCTTACAAACACGGCTACTTCTACTCGTACTGGAACGAT 354

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Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 355 GGCCACGGCGGCGTACCAATAGTGTCCGGCGGCGAGTCTCGTCAACTGGTCC 414
Qy 41 AsnSerGlyAsnPheValGlyGlySerGlyTrpGlnProGlyThrLysAsnLys----- 58
Db 415 AACTCGGGCAACTTTGTTCGGCGGCAAGGATGGCAGCCGCGCACCACCAAGAAACAGTAAGAC 474
Qy 58 ----- 58
Db 475 TACCTACCTTACCCCTTTGACCAACACAGCACACACACAATATACACACATGTGACTACC 534
Qy 59 -----ValileAsnPheSerGly 64
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Qy 65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeu 84
Db 595 AGCTACAACCCCAACCGGCAACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCTG 654
Qy 85 IleGluTyrTrpLysValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLys 104
Db 655 ATCAGTACTACATCTGTCGAGAACTTTGGCACCTTACCAACCGCTCCAGCGGCCCAACAG 714
Qy 105 HisGlyGluValThrSerAspGlySerValTyrAspLysCysArgThrGlnArgValAsn 124
Db 715 CTGGCGAGGTCACCTCCGACGGCGAGGCTACGACATTTACCGCACGCGCGGCTCAAC 774
Qy 125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArg 144
Db 775 CAGCGTCCATCATCGGCACCGCCACCTTTTACCAGTACTGGTCCGTCGCGCGCAACCAAC 834
Qy 145 ArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeu 164
Db 835 CGTCGAGCGGCTCCGTCACACCGCGCAACCACTTCAACCGCGTGGGCTCAGCAAGGCGTG 894
Qy 165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
Db 895 ACCTCGGAGCATGGATTACCAAGTTGTCGCGTGGAGGGTTACTTTAGCTCTGGCTCT 954
Qy 185 AlaSerIleThrValSer 190
Db 955 GCTTCCATCACCGTCAGC 972

RESULT 7
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LOCUS
DEFINITION
xln2-endoxylanase II [Trichoderma reesei, ALKO2721, VTT-D-79125,
Genomic, 1075 nt].
ACCESSION
S67387
VERSION
S67387.1 GI:455906
KEYWORDS
Hypocrea jecorina
SOURCE
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE
1. (bases 1 to 1075)
Saarelainen,R., Paloheimo,M., Pajestrom,R., Suominen,P.L. and
Nevalainen,K.M.
Cloning, sequencing and enhanced expression of the Trichoderma
reesei endoxylanase II (pi 9) gene xln2
Mol. Gen. Genet. 241 (5-6), 497-503 (1993)
JOURNAL
8264524
PUBMED
GenBank staff at the National Library of Medicine created this
entry [NCBI Gibbsq 140980] from the original journal article.
REMARK
Location/Qualifiers
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SITVS"
ORIGIN
Alignment Scores: 7,53e-76 Length: 1075
Pred. No.: 946.00 Matches: 179
Score: 946.00 Conservative: 4
Percent Similarity: 80.97%
Best Local Similarity: 79.20% Mismatches: 7
Query Match: 90.44% Indels: 36
DB: 15 Gaps: 1
US-09-990-874B-55 (1-190) x S67387 (1-1075)
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Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 335 GGCCACGGCGGCGTACGATACCAATGGTCCGGCGGCGAGTCTCTCGTCAACTGGTCC 394
Qy 41 AsnSerGlyAsnPheValGlyGlySerGlyTrpGlnProGlyThrLysAsnLys----- 58
Db 395 AACTCGGGCAACTTTGTTCGGCGGCAAGGGATGGACCCCGGACCAAGAACAGTAAGAC 454
Qy 58 -----ValileAsnPheSerGly 64
Db 455 TACCTACTTACCCCTTTGACCAACACAGCACACACAATATACACATGTGACTACC 514
Qy 59 -----ValileAsnPheSerGly 64
Db 515 AATCATGGATCGGATCTAACAGCTGTGTTTAAAAAAGGTCATCAACTTCTCGGA 574
Qy 65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeu 84
Db 575 AGCTACAACCCCAACCGGCAACAGCTACCTCTCGGTGTACGGCTGGTCCCGCAACCCCTG 634
Qy 85 IleGluTyrTrpLysValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLys 104
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Qy 105 HisGlyGluValThrSerAspGlySerValTyrAspLysCysArgThrGlnArgValAsn 124
Db 695 CTGGCGGAGTCACTCCGACGGCAGCGTCTACGACATTTACCGCACGCGCGCTCAAC 754
Qy 125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArg 144
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Qy 165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
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Qy 185 AlaSerIleThrValSer 190
Db 935 GCTTCCATCACCGTCAGC 952
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RESULT 8
AY320048          672 bp  mRNA  linear  PLN 14-JUL-2003
LOCUS
DEFINITION
Trichoderma viride strain YNUCC0183 endo-1,4-beta-xylanase mRNA,
complete cds.
ACCESSION
AY320048
VERSION
AY320048.1  GI:32481056
KEYWORDS
Trichoderma viride
SOURCE
Trichoderma viride
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma; Trichoderma viride species complex.
REFERENCE
1 (bases 1 to 672)
AUTHORS
Li, W.P., Zhang, Q., Liao, C.L., Zhou, J.G., Yang, Y.H., Liu, W.J. and
Yang, Z.W.
TITLE
Cloning and characterization of endo-1,4-beta-xylanase from
Trichoderma viride YNUCC0183
JOURNAL
2 (bases 1 to 672)
AUTHORS
Li, W.P., Zhang, Q., Liao, C.L., Zhou, J.G., Yang, Y.H., Liu, W.J. and
Yang, Z.W.
TITLE
Direct Submission
JOURNAL
Submitted (10-JUN-2003) Key Laboratory of Industrial Microbiology &
Fermentation Technology of Yunnan, School of Life Science, Yunnan
University, 2 North Road, Green Lake, Kunming, Yunnan 650091, China
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NINVS"
ORIGIN
Alignment Scores: 3.1e-69 Length: 672
Pred. No.: 870.00 Matches: 156
Score: 89.47% Conservative: 14
Percent Similarity: 82.11% Mismatches: 20
Best Local Similarity: 83.17% Indels: 0
Query Match: 15 Gaps: 0
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|||||
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
|||||
Db 160 GGCCATTCCGGCGTGACATACCAACCGGTGCTGGCGCTCATTCAGCGTCAACTGGGCA 219
|||||
QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlyTrpGlnProGlyThrLysAsnLysValIle 60
|||||
Db 220 AACTCGGGCAACTTTGTTCGAGGCGAAGGGATGGAACCCCGGCACTCCAGGCTCATC 279
|||||
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
|||||
Db 280 AACTTCTCTGGCAGCTACACCCCAACGGCAATAGTACCTCTCGAGTCTATGGCTGTCA 339
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QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
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Db 340 AAGAACCTCTCATCGAGTACTACATCGTTGAGAACTTTGGAACTTACACCATCGACC 399
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Db 400 GGCACACCCAGCTGGCGAGGTGACCTCTGACGGCAGCGTCTACGACATCTACCGCAGC 459
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Db 580 AACCTGGCTTGACCTCGGACCTTGGACTACGATCATTCGCGTGGAGGCTACTTTT 639
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QY 181 SerSerGlySerAlaSerIleThrValSer 190
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Db 640 AGCTCTGGTAAACCAACCACTTAACGTTAGC 669

RESULT 9
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LOCUS
DEFINITION
Trichoderma viride strain YNUCC0183 endo-1,4-beta-xylanase (XYL1)
gene, complete cds.
ACCESSION
AY370020  GI:34420135
VERSION
AY370020.1
KEYWORDS
Trichoderma viride
SOURCE
Trichoderma viride
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma; Trichoderma viride species complex.
REFERENCE
1 (bases 1 to 786)
AUTHORS
Li, W.P., Zhang, Q., Liao, C.L., Liu, S.Q., Zhou, J.G. and Liu, W.J.
TITLE
Cloning and characterization of endo-1,4-beta-xylanase from
Trichoderma viride YNUCC0183
JOURNAL
Unpublished
2 (bases 1 to 786)
AUTHORS
Li, W.P., Zhang, Q., Liao, C.L., Liu, S.Q., Zhou, J.G. and Liu, W.J.
TITLE
Direct Submission
JOURNAL
Submitted (18-AUG-2003) Key Laboratory of Industrial Microbiology &
Fermentation Technology of Yunnan, School of Life Science, Yunnan
University, 2 North Road, Green Lake, Kunming, Yunnan 650091, P.R.
China
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NINVS"
ORIGIN

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Alignment Scores: 1.51e-66 Length: 786
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Percent Similarity: 74.56% Conservative: 14
Best Local Similarity: 68.42% Mismatches: 20
Query Match: 80.40% Indels: 38
DB: 15 Gaps: 1

US-09-990-874B-55 (1-190) x AY370020 (1-786)

QY 1 GlnThrIleGlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
Db 100 CAGACGATTCGGCCCGGCACTGGCTTCAACAACGGCTACTACTCGTACTGGACGAT 159

QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyGlyPheSerValAsnTyrSer 40
Db 160 GGCCATTCGGCGTGACATACCAACGGTGCTGGCGGCTCATTCAGCGTCACTGGGCA 219

QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrPheGlnProGlyThrLys----- 56
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QY 56 ----- 56

Db 280 ACTCAAGTGAGGAACACAACTCAGATACCTCCAGACACTGGCCACCACTGCCCTGTG 339

QY 57 -----AsnLysValIleAsnPhe 62
Db 340 CCAATTCAGTCGAGAGAGCTAATACCACTCGCTGTGTAATCAAGGTCATCACTTC 399

QY 63 SerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsn 82
Db 400 TCTGGCAGCTACAAACCCCAAGGCAATAGCTACCTCTCAGTCTATGCTGGTCAAAGAAC 459

QY 83 ProLeuIleGlyTyrThrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAla 102
Db 460 CCTCTCATCGAGTACTACATCGTTGAGAACTTTGGAACTTACCAACCTCAGCGGCACC 519

QY 103 ThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArg 122
Db 520 ACCAGCTGGCGAGGAGTACTCTGACGGCAGGCTTACGACATCTACCGACGACGCGA 579

QY 123 ValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgArg 142
Db 580 GTCAACAGCGCTTCATCATCGGACCGCCACCTTTTACCAGTACTGCTGTGCGCGCG 639

QY 143 AsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrPheGln 162
Db 640 AACCAACCGCTCCAGCGGCTCGGTACCGGTTGCGAACCCTTCAACGCGTGGCGCAACCTG 699

QY 163 GlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSer 182
Db 700 GGCTTGACCTGGGAACCTTGGACTACCAATCATTCGCTGGAGGCTACTTTAGTCTCT 759

QY 183 GlySerAlaSerIleThrValSer 190
Db 760 GGTAACGCCAACATTAACTGTTAGC 783

RESULT 10
LOCUS AY156910 841 bp mRNA linear PLN 11-DEC-2002
DEFINITION Trichoderma sp. SY xylanase mRNA, complete cds.
ACCESSION AY156910
VERSION AY156910.1 GI:26514829
KEYWORDS Trichoderma sp. SY
SOURCE Trichoderma sp. SY
ORGANISM Trichoderma sp. SY
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma.
REFERENCE 1 (bases 1 to 841)
AUTHORS Min.S.Y., Kim,B.G. and Ahn,J.-H.
TITLE Purification, Characterization, and cDNA Cloning of Xylanase from

Fungus Trichoderma Strain SY
Unpublished
2 (bases 1 to 841)
Min.S.Y., Kim,B.G. and Ahn,J.-H.
Direct Submission
Submitted (30-SEP-2002) Forest and Environmental Science, Konkuk
University, 1 Hwayang-Dong, Kwangjin-Gu, Seoul 143-701, South Korea
Location/Qualifiers
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VS"

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Alignment Scores: 2.01e-66 Length: 841
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Best Local Similarity: 79.47% Mismatches: 25
Query Match: 80.31% Indels: 0
DB: 15 Gaps: 0

US-09-990-874B-55 (1-190) x AY156910 (1-841)

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Db 150 CAGGTCAATTCGGCCCGGCACTGGCTTCAACAACGGCTACTACTCGTACTGGACGAC 209

QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40
Db 210 GGCCATTCGGCGTGACTTACCAACGGCGCTGGCGGCTCTCAGCTCACTGGGCCC 269

QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrPheGlnProGlyThrLysAsnLysValIle 60
Db 270 AACTCGGCAACTTGTTCGGAGGCAAGGATGGAACCCCGGACGAGCAGCAGAACCATC 329

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSer 80
Db 330 AACTTCTCGGCACTTACAGCCCAACGACGCTACCTCTCGCTTACGGCTGGTCC 389

QY 81 ArgAsnProLeuIleGluTyrThrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
Db 390 AAGAACCCGCTCATCAGTACTACATGTGCGAAGCTTTTGGACCTTACCAACCTTCGACG 449

QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
Db 450 GGCGCCACCAAGCTGGCGAGGTGACGCTCGACGGCAGCGCTTACGACATTTACCGCAGC 509

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerVal 140
Db 510 CAGCGGCTCAACGACGCTCCATCATCGGCAACCGCCACCTTTTACCAGTACTCGTGGTG 569

QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAla 160
Db 570 CGCCGACCAACCGCTCCAGCGGCTCGGTCAACGCTGGGCAACCATCTTCAATCGCTGGCGC 629

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
Db 630 AATCTCGGCTGACGCTGGGACGAGCTACAGATTTATTGCGCTGGAGGATATTTC 689

QY 181 SerSerGlySerAlaSerIleThrValSer 190
Db 181 SerSerGlySerAlaSerIleThrValSer 190

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Db      690 AGCTCTGGCAGCGCCCAACATTACGTCAGC 719

RESULT 11
TVI012718      928 bp      mRNA      linear      PLN 15-APR-2005
LOCUS      Trichoderma viride mRNA for endo-1,4-beta-xylanase.
DEFINITION
ACCESSION      AJ012718
VERSION      AJ012718.1 GI:6434132
KEYWORDS      endo-1,4-beta-xylanase.
SOURCE      Trichoderma viride
ORGANISM      Trichoderma viride
REFERENCE
AUTHORS      Furman-Matarasso, N., Cohen, E. and Avni, A.
TITLE      Mutations in the Active Site of the Ethylene Inducing Xylanase
            Elicitor Inhibits the b-1-4-Endoxylanase Activity But Not the
            Elicitation Activity
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 928)
AUTHORS      Avni, A.
TITLE      Direct Submission
JOURNAL      Submitted (10-NOV-1998) Avni A., Plant Sciences, Tel-Aviv
            University, Tel-Aviv University, Tel-Aviv, 69978, ISRAEL
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Percent Similarity:      89.01%      Conservative:      14
Best Local Similarity:      81.68%      Mismatches:      20
Query Match:      79.73%      Indels:      2
DB:      15      Gaps:      0

US-09-990-874B-55 (1-190) x TVI012718 (1-928)

Qy      1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
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Qy      21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db      222 GGCCATTCCGGCGTGACATACACCAACGCTGCGGCTCATTCAGCGTCACTGGGCA 281
Qy      41 AsnSerGlyAsnPheValGlyGlyGlyTrpGlnProGlyThrLysAsnLysValIle 60
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Qy      61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80

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Db      342 AACTTCTCTGCGAGCTACAAACCCCAACGGCAACAGCTACCTCTCAGTCTATGGTGGTCC 401
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Qy      121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
Db      522 CAGCGAGTCAACAGCGCTTCATCATCGGAACGGCCACCTTTTACCAGTAGTACTGGTCTGTC 581
Qy      141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPhe-AsnAlaTrpAl 160
Db      582 CGCGCAACCA-CCGCTCCAGCGGCTCGGTCCACGGTTCGGAACCACTTCCACACGGGTGGCG 640
Qy      160 aArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPh 180
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Qy      180 eSerSerGlySerAlaSerIleThrValSer 190
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LOCUS      Chaetomium gracile endo-beta1,4-xylanase B (cgxB) gene, complete
DEFINITION
ACCESSION      D49851
VERSION      D49851.1 GI:1339859
KEYWORDS      cgxB; endo-beta1,4-xylanase.
SOURCE      Chaetomium gracile
ORGANISM      Chaetomium gracile
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
REFERENCE
AUTHORS      Yoshino, S., Oishi, M., Moriyama, R., Kato, M. and Tsukagoshi, N.
TITLE      Two family G xylanase genes from Chaetomium gracile and their
            expression in Aspergillus nidulans
JOURNAL      Curr. Genet. 29 (1), 73-80 (1995)
PUBMED      8595661
REFERENCE      2 (bases 1 to 2208)
AUTHORS      Tsukagoshi, N.
JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 2208)
AUTHORS      Tsukagoshi, N.
TITLE      Direct Submission
JOURNAL      Submitted (25-MAR-1995) Norihiro Tsukagoshi, Nagoya University,
            Faculty of Agriculture, Applied Biological Sciences, Furo-cho,
            Chikusa-ku, Nagoya, Aichi 464-01, Japan
            (E-mail: i45370a@nuecc.cc.nagoya-u.ac.jp, Tel: 052-789-4086,
            Fax: 052-789-4087)
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exon
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exon

ORIGIN

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Best Local Similarity: 65.33% Mismatches: 30
Query Match: 69.12% Indels: 16
DB: 15 Gaps: 1

US-09-990-874B-55 (1-190) x CEMXB2 (1-2208)

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Db 898 ACTGGACCAACACCGCTACTACTCTGCTTCTGGACTGACGCCAGGCGACGTCAG 957
Qy 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
Db 958 TACACCAACGAGGCTGGGGCCAGTACAGCGTGAGCTGGTGGGCAACGCNATGGGTC 1017
Qy 47 GlyGlyLysGlyTrpGlnProGlyThrLysAsn----- 57
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Qy 58 -----LysValIleAsnPheSerGlySerTyrAsnProAsnGly 70
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Qy 71 AsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIleGluTyrIleVal 90
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Db 1198 GAGAACTTTGGCAGCTACACCCCTCGACGGCGCCACCGCGTGGCGCGTGCAGCACC 1257
Qy 111 AspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGluGly 130
Db 1258 GACGGGTCTTGTACGACATCTACCGCACGCGCGCTCAACCGCGCTCGATCGAGGGT 1317
Qy 131 ThrAlaThrPheTyrGlnTyrTrpSerValArgArgAsnArgSerSerGlySerVal 150
Db 1318 ACCAGACCTTCTACCAATTTCTGGTGGTGCGCCAGAACAGCGCACCGCGCGCAGCGTC 1377
Qy 151 AsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAsp 170
Db 1378 AACATGCGCCGCCACTTCAACGCGCTGGCGCGCGCGCTGCGAGCTGGCGCACCCACGAC 1437
Qy 171 TyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThrVal 189
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RESULT 13
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LOCUS NCB8G12 154038 bp DNA linear PLN 17-APR-2005
DEFINITION Neurospora crassa DNA linkage group V BAC contig B8G12.

ACCESSION BX294027

VERSION BX294027.1 GI:28950191

KEYWORDS

SOURCE Neurospora crassa

ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariales; Neurospora.

REFERENCE

AUTHORS

JOURNAL

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

gene

CDS

exon

intron

exon

gene

gene

CDS

1 Schulte,U., Aign,V., Hoheisel,J., Brandt,P., Fartmann,B.,
Holland,R., Nyakatura,G., Mewes,H.W. and Mannhaupt,G.
2 Unpublished
2 (bases 1 to 154038)
German Neurospora genome project.
Submitted (11-MAR-2003) MIPS, Institut fuer Bioinformatik,
GSP-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,
Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:
G.Mannhaupt@gf.de Project Coordinator: Ulrich Schulte, Institute
of Biochemistry, Heinrich-Heine-University, D-40225 Dueseldorf,
E-mail: ulrich-schulte@uni-dueseldorf.de
this contig is an assembly of BAC 8G12 from 1 to: 79514, cosmid
6585 from 79515 to: 119973 and BAC 7L15 from 119974 to:154038; BACS
74-OR-23-1A) are available at the Fungal Genetic Stock Center,
http://www.fgsc.net Sequencing was performed by MWG Biotech AG,
Ebersberg, Germany, http://www.mwgdna.com
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of linkage groups II
and V can be viewed at: http://mips.gsf.de/proj/neurospora.

Location/Qualifiers

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11 active sites signatures, Glycosyl Hydrol F11 2
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QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
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QY 121 GluArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
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Db 3320 AGTCCGGTCTCAGCTCGCGCACCACTACAGATTGTTGCTACCGAGGATATTT 3261
QY 181 SerSerGlySerAlaSerIleThrVal 189
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RESULT 14
LOCUS AR149835 1281 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6228629.
ACCESSION AR149835
VERSION AR149835.1 GI:15114426
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1281)
AUTHORS Palohelimo,M., Hakola,S., Mantyla,A., Vehmaanpera,J., Lantto,R.,
Lahtinen,T., Fagerstrom,R.B. and Suominen,P.
TITLE Xylanases, genes encoding them, and uses thereof
JOURNAL Patent: US 6228629-A 1 08-MAY-2001;
FEATURES
Location/Qualifiers
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Best Local Similarity: 60.00% Mismatches: 36
Query Match: 65.68% Indels: 22
DB: 6 Gaps: 2

US-09-990-874b-55 (1-190) x AR149835 (1-1281)

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QY 20 AspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrp 39
Db 333 GATGGCCAAAGGCAACATTCGCTTCAACCTCGAGCGGTGGCCAGTACACGCGTACATGG 392
QY 40 SerAsnSerGlyAsnPheValGlyGlyLys----- 49
Db 393 TCTGGTAAAGGCAACTGGGTGGCGGCA--AGGTATGTCTCTTTAATGTTCCAGCGCTA 451
QY 50 -----GlyTrpGlnProGlyThrLysAsnLysVal 59
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QY 80 SerArgAsnProLeuIleGluTyrThrIleValGluAsnPheGlyThrTyrAsnProSer 99
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QY 100 ThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArg 119
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Db 752 GTGCGCACCTCCAAAGCGCACCGCGGTACTGTTACCATGGCCCAACCACTTCAATGCTTG 811
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Db 812 AGCAGGCTGGTCTGCAGCTGGGTTCCTCATGATTATCAGATTGTGGCTACTGAGGGTTAC 871
QY 180 PheSerSerGlySerAlaSerIleThrVal 189
Db 872 TACTCTCTGGCTCGCGGACTGTCAATGTT 901

RESULT 15
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DEFINITION Sequence 1 from Patent EP1433843.
ACCESSION CQ847410
VERSION CQ847410.1 GI:51469070
KEYWORDS
SOURCE Chaetomium thermophilum
ORGANISM Chaetomium thermophilum
REFERENCE 1
AUTHORS Palohelimo,M., Hakola,S., Maentyla,A., Vehmaanpera,J., Lantto,R.,
Lahtinen,T., Fagerstrom,R. and Suominen,P.
TITLE Novel xylanases, genes encoding them, and uses thereof
JOURNAL Patent: EP 1433843-A 1 30-JUN-2004;
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Pred. No.: 1.94e-52 Length: 1281
Score: 687.00 Matches: 126
Percent Similarity: 72.86% Conservative: 27
Best Local Similarity: 60.00% Mismatches: 36
Query Match: 65.68% Indels: 22
DB: 6 Gaps: 2

US-09-990-874b-55 (1-190) x CQ847410 (1-1281)

QY 1 GlnThrIle---GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsn 19
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Qy      50  -----GlyTTPGlnProGlyThrLysAsnLysVal 59
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Qy      100  ThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArg 119
Db      632  ACGGGCGCCACCCGATCGGCGAGCGGTGACACCGAGCGGCGGACCTACACATCTACCGC 691
Qy      120  ThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTTPSer 139
Db      692  ACGCAGCGCGTCAACGCGCCCTCCATCGAGGGCCACCAAGACCTTCTACCAATACTGGTCT 751
Qy      140  ValArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTTP 159
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Qy      160  AlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
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Search completed: December 30, 2005, 02:30:36
Job time : 3281 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2005, 19:17:01; Search time 474 Seconds

(without alignment)
2671.501 Million cell updates/sec

Title: US-09-990-874B-55

Perfect score: 1046

Sequence: 1 QTIQPGTGYDGYFSYWN.....YQIVAVEGYFSSGSASITVS 190

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Database :

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- 3: Geneseq2000s:*
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- 14: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	974	93.1	596	6 AAD29410	Aad29410 Trichoder
3	974	93.1	596	9 AAL60925	Aal60925 Trichoder
4	974	93.1	596	9 AAL60941	Aal60941 Trichoder

5	948	90.6	573	2 AAV36098	AAV36098 DNA seque
6	946	90.4	1015	2 AAQ54775	AAQ54775 T. reesei
7	946	90.4	1015	2 AAV81332	AAV81332 T. reesei
8	919	87.9	822	2 AAV29598	AAV29598 DNA seque
9	687	65.7	1281	2 AAT71585	AAT71585 Chaetomiu
10	664.5	63.5	705	10 ABQ80364	ABQ80364 A. fumiga
11	648	62.0	739	10 ABQ80363	ABQ80363 A. fumiga
12	643.5	61.5	588	5 AAS13813	AAS13813 DNA encod
13	643.5	61.5	678	4 AAD17927	AAD17927 Thermomyc
14	643.5	61.5	983	2 AAT40742	AAT40742 Xylanase
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18	638.5	61.0	1273	2 AAQ90388	AAQ90388 Xylanase
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36	598	57.2	1008	12 ADJ35015	ADJ35015 DNA encod
37	593	56.7	1195	2 AAZ28864	Aaz28864 Streptomy
38	593	56.7	1195	2 AAZ28865	Aaz28865 Streptomy
39	591	56.5	1047	12 ADJ35083	ADJ35083 DNA encod
40	590.5	56.5	1338	12 ADJ35151	ADJ35151 DNA encod
41	590	56.4	1044	12 ADJ34979	ADJ34979 DNA encod
42	589.5	56.4	1077	12 ADJ34965	ADJ34965 DNA encod
43	584.5	55.9	2225	4 AAS13689	Aas13689 Gene enco
44	584	55.8	576	10 ADK70798	ADK70798 Streptomy
45	581.5	55.6	1085	12 ADJ34999	ADJ34999 DNA encod

ALIGNMENTS

RESULT 1
AAA48219
ID AAA48219 standard; cDNA; 596 BP.

XX
AC AAA48219;
XX
DT 15-SEP-2003 (revised)
DT 28-SEP-2000 (first entry)
XX

T. reesei xylanase, Xyn II, coding sequence, Trx.

Xylanase; animal feed; digestion efficiency; thermostable;

feed pelleting; enzyme; Trx; XyTV-101; XyTV-102; Trx-103; XyTV-104;

XyTV-105; XyTV-106; XyTV-107; Trx-108; XyTV-109; Xyn A; Xyn B;

Xyn; Xyn C; Xyn I; Xyn II; ss.

Hypocrea jecorina.

XX Key Location/Qualifiers
XX CDS 23..594
FT /*tag= a
FT /partial
FT /product= "Trx"
XX

WO200029587-A1.

XX 25-MAY-2000.

XX

PF 16-NOV-1999; 99WO-CA001093.
 XX
 PR 16-NOV-1998; 98US-0108504P.
 XX
 PA (IOGE-) IOGEN CORP.
 XX
 PI Sung WL, Tolan JS;
 XX
 DR WPI; 2000-387799/33.
 DR P-PSDB; AAY99680.
 XX
 PT Thermostable xylanases useful for preparing animal feeds especially
 PT poultry or swine feed, exhibits optimal activity under physiological
 PT conditions.
 XX
 PS Example 1; Fig 2; 86pp; English.
 XX
 CC Xylanase enzymes are added to animal feeds to increase the efficiency of
 CC digestion and assimilation of nutrients. Xylanases are preferentially
 CC added during the feed pelleting process. To survive the pelleting process
 CC and to have optimum activity in the animal, the xylanase needs to have
 CC high thermostability, with optimum activity at physiological pH and
 CC temperature. Various xylanases have some properties suitable for feed
 CC applications but they lack the thermostability required to survive food
 CC pelleting. The present sequence is the coding sequence for xylanase Trx,
 CC which was derived from *Trichoderma reesei*. This coding sequence was
 CC constructed from 18 overlapping oligonucleotides: XyTV-101 (AAA48229),
 CC XyTV-102 (AAA48230), Trx-103 (AAA48231), XyTV-104 (AAA48232), XyTV-105
 CC (AAA48233), XyTV-106 (AAA48234), XyTV-107 (AAA48235), Trx-108 (AAA48236),
 CC XyTV-109 (AAA48237), XyTV-110 (AAA48238), Trx-111 (AAA48239), XyTV-2
 CC (AAA48240), Trx-3 (AAA48241), XyTV-4 (AAA48242), Trx-5
 CC (AAA48243), XyTV-7 (AAA48244), Trx-8 (AAA48245). This sequence was
 CC mutated to produce mutant xylanases with enhanced thermostability
 CC (AAY99683, AAY99684, AAY99685, AAY99686, AAY99735 and AAY99736) which
 CC would be useful for animal feeds, especially poultry and swine feed.
 CC (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 596 BP; 175 A; 131 C; 140 G; 150 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,35e-94 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.12% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 3 Gaps: 0

US-09-990-874B-55 (1-190) x AAA48219 (1-596)

Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
 Db 23 CAACAATACACACCGAGAACCGGTTACACACGGTTACTTTTACAGCTATGGACGAT 82
 Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 Db 83 GGCCATGGTGGTGTACTTATACAAACGGCCGGCCGAGGCCAATTAGGCTCAATTGGTCT 142
 Qy 41 AsnSerGlyAsnPheValGlyGlyLysGlyTrpGlnProGlyThrLysAsnLysValIle 60
 Db 143 AACTCCGGAACCTTCGTAGGTGGAAGAGGTTGGCAACCCGGGACCCAAATAAGGTGATC 202
 Qy 61 AsnPheSerGlySerTyrAsnProAsnGlnVAnSerTyrLeuAlaValTyrGlyTrpSer 80
 Db 203 AACTTCTCTGGATCTTAAATCCGAATCGGAATTCATACTTAAGGCTCTATGGCTGGTCT 262
 Qy 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 Db 263 AGAAACCCACTGATTGATATATACATTCGGAATTTTCGGTACTACATCCGAGTACC 322
 Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 Db 323 GGCGCCACANAATTAGCGCAAGTCACTAGTGTATGGATCCGTATATATATATATACCGTACC 382

Qy 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
 Db 383 CAACGGCTTAAATCAGCCATCGATCATTTGGAAACCGCCACCTTTTATCATGACTCGAGTGT 442
 Qy 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 Db 443 AGACGTAATCATCGGAGCTCCGGTTCGGTTAAATCACTCGAATCACTTAAATGCAATGGCA 502
 Qy 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 Db 503 CAGCAGGGTTACCCCTAGGTACATGATTAATCAATCGTAGCGGTGGAGGCTACTTTC 562
 Qy 181 SerSerGlySerAlaSerIleThrValSer 190
 Db 563 TCGAGTGGTTCGGCTAGTATTACAGTGAGC 592

RESULT 2
 AAD29410
 ID AAD29410 standard; DNA; 596 BP.
 XX
 AC AAD29410;
 XX
 DT 29-AUG-2003 (revised)
 DT 16-MAY-2002 (first entry)
 XX
 DE *Trichoderma reesei* xylanase (Trx), Xyn II DNA.
 XX
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;
 KW pulp manufacture; poultry; swine feed; enzyme; Xyn II; ds.
 XX
 OS *Hypocrea jecorina*.
 XX
 FH Key Location/Qualifiers
 FT CDS 23..595
 FT /*tag= a
 FT /product= "Trx Xyn II"
 FT /note= "CDS does not include start codon"
 FT /partial
 XX
 FN WO200192487-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 31-MAY-2001; 2001WO-CA000769.
 XX
 PR 31-MAY-2000; 2000US-0213803P.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Sung WL;
 XX
 DR WPI; 2002-171435/22.
 DR P-PSDB; AAE18452.
 XX
 PT Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing.
 XX
 FS Example 1; Page 88; 109pp; English.
 CC
 CC The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also
 CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermostability and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is *Trichoderma reesei*
 CC xylanase (Trx), Xyn II DNA. (Updated on 29-AUG-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 596 BP; 175 A; 131 C; 140 G; 150 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,35e-94 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x AAD29410 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
 DB 23 CAACAATAACACCGGACCGGTTACAAACCGGTACTTTTACAGCTATTGGACGAT 82
 QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 DB 83 GGCATGTTGGTGTACTTACATAACACCGGCGGAGCCCAATTAGCGTCAATTGGTCT 142
 QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValile 60
 DB 143 AACTCCGGAACCTTCGTAGGTGGAAGGTTGGCAACCGGACCAAAAATAAGGTGATC 202
 QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
 DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATACCTTAAGCGTCTATGGCTGCT 262
 QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 263 AGAACCACCTGATTGATATACATTGTTCGAAAATTTCCGTACTACATCCGAGTACC 322
 QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 323 GGCGCCACAAAATTAGCGAAGTCACTAGTGTGATGATCGGTATATGATATCTACCGTACC 382
 QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
 DB 383 CAACGGGTTAATCAGCCATCGATCATTTGGAACCGCCACCTTTTATCATGTAGTACGAGTGT 442
 QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 DB 443 AGACGTAAATCATCGGAGCTCCGGTTCGGTTAATCTACTGCGGAGGCACTCTTC 502

RESULT 3

AAL60925
 ID AAL60925 standard; DNA; 596 BP.

AC AAL60925;
 XX
 DT 27-OCT-2003 (revised)
 DT 03-SEP-2003 (first entry)
 XX
 DE Trichoderma reesei xylanase II enzyme (Trx) gene #1.
 XX
 KW Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
 KW pulp manufacture; poultry feed; swine feed; enzyme; gene; ds.
 XX
 OS Hypocrea jecorina.
 XX
 FH Key Location/Qualifiers
 FT 23...595
 FT CDS
 FT /*tag= a
 FT /product= "T. reesei xylanase II enzyme (Trx)"
 FT /note= "CDS does not include start codon"
 FT /partial
 XX

PN WO2003046169-A2.
 XX
 PD 05-JUN-2003.
 XX
 PP 20-NOV-2002; 2002WO-CA001758.
 XX
 PR 21-NOV-2001; 2001US-00990874.
 XX
 XX (CANA) NAT RES COUNCIL CANADA.
 XX
 XX Sung WL;
 XX
 XX WPI; 2003-513647/48.
 DR P-PSDB; AAO30259.

Novel modified xylanase useful in industrial process, exhibits improved thermophilicity, alkalophilicity and expression efficiency, in comparison to a corresponding native xylanase from *Trichoderma reesei*.
 Example 1; Fig 2; 105pp; English.

The invention relates to modified xylanase enzyme which exhibits improved thermophilicity, alkalophilicity and expression efficiency, in comparison to a corresponding native *Trichoderma reesei* xylanase (Trx). The modified xylanase is useful in an industrial process e.g. pulp manufacturing. It is useful for the bleaching of pulp, processing of precision devices and for improving digestibility of poultry and swine feed. The present sequence is *Trichoderma reesei* xylanase II enzyme encoding gene. (Updated on 27-OCT-2003 to standardise OS field)

Sequence 596 BP; 175 A; 131 C; 140 G; 150 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,35e-94 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x AAL60925 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
 DB 23 CAACAATAACACCGGACCGGTTACAAACCGGTACTTTTACAGCTATTGGACGAT 82
 QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 DB 83 GGCATGTTGGTGTACTTACATAACACCGGCGGAGCCCAATTAGCGTCAATTGGTCT 142
 QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValile 60
 DB 143 AACTCCGGAACCTTCGTAGGTGGAAGGTTGGCAACCGGACCAAAAATAAGGTGATC 202
 QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
 DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATACCTTAAGCGTCTATGGCTGCT 262
 QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 263 AGAACCACCTGATTGATATACATTGTTCGAAAATTTCCGTACTACATCCGAGTACC 322
 QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 323 GGCGCCACAAAATTAGCGAAGTCACTAGTGTGATCGGTATATGATATCTACCGTACC 382
 QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
 DB 383 CAACGGGTTAATCAGCCATCGATCATTTGGAACCGCCACCTTTTATCATGTAGTACGAGTGT 442
 QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 DB 443 AGACGTAAATCATCGGAGCTCCGGTTCGGTTAATCTACTGCGGAGGCACTCTTC 502

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 503 CAGCAGGGTTAACCTAGGTACATCGATGGATTATCAATCGTAGCGTGGAGGCTACTTC 562

QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 563 TCGAGTGGTTCGCTAGTATTACAGTGAGC 592

RESULT 4
 AAL60941/c
 ID AAL60941 standard; DNA; 596 BP.
 AC AAL60941;
 XX
 DT 27-OCT-2003 (revised)
 DT 03-SEP-2003 (first entry)
 XX
 DE Trichoderma reesei xylanase II enzyme (Trx) gene #2.
 XX
 KW Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
 KW pulp manufacture; poultry feed; swine feed; enzyme; gene; ds.
 XX
 OS Hypocrea jecorina.
 XX
 PN W02003046169-A2.
 XX
 PD 05-JUN-2003.
 XX
 XX 20-NOV-2002; 2002WO-CA001758.
 PF
 XX 21-NOV-2001; 2001US-00990874.
 PR
 XX (CANADA) NAT RES COUNCIL CANADA.
 PA
 XX Sung WL;
 PI
 XX WPI; 2003-513647/48.
 DR
 XX
 PT Novel modified xylanase useful in industrial process, exhibits improved
 PT thermophilicity, alkalophilicity and expression efficiency, in comparison
 PT to a corresponding native xylanase from Trichoderma reesei.
 XX
 PS Example 1; Fig 2; 105pp; English.
 XX
 CC The invention relates to modified xylanase enzyme which exhibits improved
 CC thermophilicity, alkalophilicity and expression efficiency, in comparison
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
 CC is useful for the bleaching of pulp, processing of precision devices and
 CC for improving digestibility of poultry and swine feed. The present
 CC sequence is Trichoderma reesei xylanase II enzyme encoding gene. (Updated
 CC on 27-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 596 BP; 150 A; 140 C; 131 G; 175 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,35e-94 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 9 Gaps: 0

US-09-990-874B-55 (1-190) x AAL60941 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
 DB 578 CAACACATACACACACGAGAACCGGTTCACACACGGTTACTTTTACAGTATTGGACGAT 519

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSer 40
 DB 518 GGCCATGGTGGTGTACCTATACACACGGGCGGAGGCCAATTTAGCGTCAATTGGTCT 459

QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrIysAsnLysValIle 60
 DB 458 AACTCCGGAACTTCGTAGGTGGAAAGGTTGGCAACCCCGGACCAAAAATAAGGTGATC 399

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrIleuAlaValTyrGlyTrpSer 80
 DB 398 AACTTCTCTCGATCTTATATAATCCGAATGGGAATTCATACTTAAGCGTCTATGGCTGGTCT 339

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 338 AGAACCCTGATTTGATATATACATTTGCGAAAATTTTCGGTACCTACCAATCCGAGTACC 279

QY 101 GlyAlaThrIlyHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 278 GGGCCACAAAATTAGCGGAAGTCACTAGTAGTGGATCCGTATATATATCTACCGTACC 219

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
 DB 218 CAACGGCTTAATCAGCCATCGATCATTTGGAAACCGCCACCTTTTATCATGACTGGAGTGT 159

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 DB 158 AGAGTAAATCATCGAGCTCCGGTTCGGTTAATCTCGGAATCACTTTAATGCAATGGCA 99

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 98 CAGCAGGGTTAACCTAGGTACATCGATTATCAATCGTAGCGTGGAGGCTACTTTC 39

QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 38 TCGAGTGGTTCGCTAGTATTACAGTGAGC 9

RESULT 5
 AAV36098
 ID AAV36098 standard; DNA; 573 BP.
 AC AAV36098;
 XX
 DT 02-SEP-1998 (first entry)
 XX
 DE DNA sequence of the specification.
 XX
 KW Family 11 xylanase; improve; thermophilicity; alkalophilicity;
 KW thermotolerance; bleach; wood pulp; processing; wheat; maize;
 KW digestibility-improving animal feed additive; starch production; mutant;
 KW ds.
 XX
 OS Synthetic.
 XX
 PN EP828002-A2.
 XX
 PD 11-MAR-1998.
 XX
 XX 05-SEP-1997; 97EP-00115412.
 XX
 XX 09-SEP-1996; 96US-00709912.
 XX
 XX (CANADA) NAT RES COUNCIL CANADA.
 XX
 XX Sung WL, Yaguchi M, Ishikawa K;
 XX WPI; 1998-161100/15.
 XX
 XX Modified xylanase enzymes - useful for improving wood pulp bleaching,
 XX etc.
 PS
 PS Disclosure; Page 50; 84pp; English.
 XX
 CC The present sequence appears in the specification, which describes a
 CC method for modifying a Family 11 xylanase to improve its thermophilicity,
 CC alkalophilicity and or thermotolerance. This method comprises
 CC modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase

CC 11 or corresponding aligned amino acids of another Family 11 xylanase,
 CC replacement of one or more amino acid sequences in the N-terminal region
 CC with corresponding aligned sequences from another Family 11 xylanase to
 CC form a chimeric xylanase and/or upstream extension of the N terminus by
 CC addition of upto 10 amino acids. The modified xylanases are useful for
 CC improving the bleaching of wood pulp by treatment at 55-75 degrees
 CC Celsius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as
 CC digestibility-improving animal feed additives. They might also be useful
 CC in the processing of wheat or maize for starch production
 XX
 SQ Sequence 573 BP; 163 A; 127 C; 136 G; 147 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.33e-91 Length: 573
 Score: 948.00 Matches: 174
 Percent Similarity: 95.24% Conservative: 6
 Best Local Similarity: 92.06% Mismatches: 9
 Query Match: 90.63% Indels: 0
 DB: 2 Gaps: 0

US-09-990-874B-55 (1-190) x AAV36098 (1-573)

QY 2 ThrileGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrPheAsnAspGly 21
 DB 3 AGCATAGGACGAGGACCGGTTTCAACACACGGTTTACTTTTACAGCTATTGGACGATGGC 62
 QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsn 41
 DB 63 CATGGTGGTGTACTTATACAAACGGCCCGAGGCCAATTAGCGTCAATTGGTCTTAAC 122
 QY 42 SerGlyAsnPheValGlyGlyLeuGlyTyrTrpGlnProGlyThrLysAsnLysValIleAsn 61
 DB 123 TCCGGAACATTCGTAGTGGAAAGGTTGGCAACCGCGGACCAAAATAAGTGTATCAAC 182
 QY 62 PheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
 DB 183 TTCTCTGGATCTTATAATCCGAATGGGAATTCATACCTTAAGCGTCTATGGTGTCTAGA 242
 QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGly 101
 DB 243 AACCCACTGATTGAATATTACATTTGCGAAATTTCCGTACCTCAATCCGAGTACCGGC 302
 QY 102 AlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGln 121
 DB 303 GCCACAAATTAAGCGAAGTCACTAGTAGGATCCGTATATGATATCTACCGTACCCAA 362
 QY 122 ArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArg 141
 DB 363 CGCGTTAATCAGCCATCGATCATTTGGAACCGCCACCTTTTATCAGTACTGCGAGTGTAGA 422
 QY 142 ArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArg 161
 DB 423 CGTACGCATCCGAGCTCCGGTTCGGTTAACTTCGGAATCACTTTAATGATGGGCACAG 482
 QY 162 GlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSer 181
 DB 483 CAAGGTTAACCCTAGGTACATGGATATCAATTCGTAGCGTGGAGGCTACTTCTCG 542
 QY 182 SerGlySerAlaSerIleThrValSer 190
 DB 543 AGTGGTTCGCTAGTATTACAGTGAGC 569

RESULT 6

AAQ54775

ID AAQ54775 standard; DNA; 1015 BP.

XX

AC AAQ54775;

XX 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 10-JUN-1994 (first entry)

XX

DE T. reesei xln2 gene.

XX Trichoderma reesei; enzyme; paper; pulp; food; feed industry; pi 5.5;
 KW pi 9.0; xln1; xln2; endoxylanase; ss.
 XX Hypocrea jecorina; QM6a.
 XX
 FH Key Location/Qualifiers
 FT TATA_signal 36..41
 FT CDS 176..955
 FT /tag= a
 FT /tag= b
 FT mat_peptide 275..952
 FT /tag= d
 FT intron 449..556
 FT /tag= c
 XX
 XX WO9324621-A1.
 XX 09-DEC-1993.
 XX 24-MAY-1993; 93WO-FI000221.
 XX 29-MAY-1992; 92US-00889893.
 XX (ALKO-) ALKO OY AB.
 XX
 XX Suominen P, Nevalainen H, Saarelainen R, Paloheimo M, Lahtinen T;
 PI Pagarstroem R;
 XX
 DR WPI; 1993-405812/50.
 DR P-PSDB; AAR47122.
 PT Isolated nucleic acid mol. used in enzymes for paper, pulp and feed
 PT industry - comprising sequence encoding aminoacid sequence of T. reesei
 PT pi 5.5 xylanase.
 XX
 PS Claim 4; Page 77-78; 111pp; English.
 XX

CC The T. reesei xln2 gene coding for the pi 9.0 endoxylanase was isolated
 CC from the wild-type strain QM6a. The gene contains one intron of 108
 CC nucleotides and codes for a protein of 223 amino acids in which two
 CC putative N-glycosylation target sites were found. Three different T.
 CC reesei strains were transformed by targeting a construct composed of the
 CC xln2 gene with its own promoter to the endogenous cbh1 locus. Highest
 CC overall prodn. levels for xylanase were obtained using the T. reesei
 CC ALK02721, a genetically engineered strain, as a host. Integration into
 CC the cbh1 locus was not required for enhanced expression under xln2
 CC promoter. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-
 CC MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS
 CC field)

SQ Sequence 1015 BP; 261 A; 328 C; 240 G; 186 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.59e-91 Length: 1015
 Score: 946.00 Matches: 179
 Percent Similarity: 80.97% Conservative: 4
 Best Local Similarity: 79.20% Mismatches: 7
 Query Match: 90.44% Indels: 36
 DB: 2 Gaps: 1

US-09-990-874B-55 (1-190) x AAQ54775 (1-1015)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrPheAsnAsp 20
 DB 275 CAGACGATTGAGCCCGGCGGCTACACACACGGCTACTTCTACTCGTACTGGAACGAT 334
 QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSer 40
 DB 335 GGCCACGGCGGCGTGCATACCAATGGTCCCGGGGCGAGTTCCTCCGCAACTGGTCC 394
 QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrTrpGlnProGlyThrLysAsnLys----- 58

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Db 395 AACTCGGGCAACTTTTGTTCGGCGCAAGGATGGCAGCCCGGGACCAAGAAAGTAAGAC 454
QY 58 ----- 58
Db 455 TACCTACTCTTACCCCTTTTGACCAACACAGCACAACAATACACATGTGACTACC 514
QY 59 -----ValleAsnPheSerGly 64
Db 515 AATCATGGAATCGGATCTAACAGCTGTGTTTTTAAAAAAGGGTCATCAACTTCTCGGA 574
QY 65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeu 84
Db 575 AGCTACAAACCCCAACGGCAACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCTG 634
QY 85 IleGluTyrTrilleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrlys 104
Db 635 ATCAGGTACTACATCGTCGAGAACTTTGGCACTTACACCCGTCCACGGGGCCACCAG 694
QY 105 HisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsn 124
Db 695 CTGGCGGAGGTCACTCCGACGGCAGCGTCTACGACATTTACCGCAGCAGCGGTCAAC 754
QY 125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArg 144
Db 755 CAGCGGTCCATCATCGGCAGCCGACCTTTTACCAGTACTGGTCCGTCCGCGCAACCCAC 814
QY 145 ArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGlnGlyLeu 164
Db 815 CGCTCGAGCGGCTCCGTTCACACGGCGAACCACTTCAACGGCTGGGCTCAGCAAGGCGCTG 874
QY 165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
Db 875 ACGTCTGGGACGATGATTACAGATTTGCGCGTGGAGGTACTTTAGTCTGGCTCT 934
QY 185 AlaSerIleThrValSer 190
Db 935 GCTTCCATCACCGTCAGC 952

RESULT 7
AAV81332
ID AAV81332 standard; DNA; 1015 BP.
XX AC
XX AAV81332;
AC
DT 17-OCT-2003 (revised)
DT 02-MAR-1999 (first entry)
XX
XX T. reesei xylanase II gene.
XX
XX Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;
XX degradation; polymer; xylan; carbohydrate; plant; paper; pulp; ss.
XX
XX Hypocrea jecorina.
XX
XX Key Location/Qualifiers
XX TATA_signal 36..42
XX /*tag= a
XX CDS 176..955
XX /*tag= b
XX /gene= "xln2"
XX /product= "xylanase 2"
XX /note= "CDS contains an intron"
XX sig_peptide 176..232
XX /*tag= c
XX /note= "primary signal peptide sequence"
XX sig_peptide 233..275
XX /*tag= d
XX /note= "propeptide sequence"
XX mat_peptide 275..952
XX /*tag= e
XX intron 449..556
XX /*tag= f
XX /cons_splice= (5'site:NO, 3'site:NO)
```

```
XX US8837515-A.
FN
XX 17-NOV-1998.
PD
XX 16-SEP-1993; 93US-00121436.
PF
XX 16-MAY-1990; 90US-00524308.
PR 29-MAY-1992; 92US-00889893.
PR 24-MAY-1993; 93WO-FI000221.
PR 18-JUN-1993; 93US-00078478.
XX (ALKO-) ALKO-YHTIOET OY.
XX
XX Paloheimo M, Nevalainen H, Saarelainen R, Fagerstroem R,
PI Suominen P;
XX
XX WPI; 1999-023453/02.
DR P-PSDB; AAW67567.
XX
XX Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for
PT recombinant production of the enzyme, for use in paper and pulp
PT production.
XX
XX Claim 4; Fig 3A-B; 52pp; English.
XX
XX This sequence corresponds to the gene encoding the Trichoderma reesei
CC xylanase II enzyme (xln2) which has an isoelectric point (pI) of 9. The
CC sequence was isolated by reverse transcription PCR using the primers
CC AAV81333-V81335 based on amino acid sequence derived from the N-terminal
CC of the purified protein. The encoded protein contains a 33 amino acid
CC propeptide sequence with a primary signal peptide cleavage site between
CC residues 19-20. The mature protein comprises 190 amino acids with a
CC calculated molecular weight of 20.8 kD. The enzymes are used in the
CC degradation of the polymer xylan, one of the most abundant carbohydrate
CC components in plants. This is especially useful in the paper and pulp
CC making industry. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 1015 BP; 261 A; 328 C; 240 G; 186 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.59e-91 Length: 1015
Score: 946.00 Matches: 179
Percent Similarity: 80.97% Conservative: 4
Best Local Similarity: 79.20% Mismatches: 7
Query Match: 90.44% Indels: 36
DB: 2 Gaps: 1

US-09-990-874B-55 (1-190) x AAV81332 (1-1015)
QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
Db 275 CAGACGATTTCAGCCCGGACGCGGTACACACACGGCTACTTCTACTGTGTAAGACGAT 334
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40
Db 335 GGCCACGGCGGCGTGACGTACACCAATGGTCCCGCGGCGAGTTCTCCGTCAACTGGTCC 394
QY 41 AsnSerGlyAsnPheValGlyGlyGlyTyrGlnProGlyThrIleAsnLys----- 58
Db 395 AACTCGGGCAACTTTTGTTCGGCGCAAGGATGGCAGCCCGGGACCAAGAAAGTAAGAC 454
QY 58 ----- 58
Db 455 TACCTACTCTTACCCCTTTTGACCAACACAGCACAACAATACACATGTGACTACC 514
QY 59 -----ValleAsnPheSerGly 64
Db 515 AATCATGGAATCGGATCTAACAGCTGTGTTTTTAAAAAAGGGTCATCAACTTCTCGGA 574
QY 65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeu 84
Db 575 AGCTACAAACCCCAACGGCAACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCTG 634
```


QY 85 IleGluTyrTrpValGluAlaPheGlyThrTyrAsnProSerThrGlyAlaThrIys 104
 DB 635 ATCCAGTACTACCTGTCGAGACTTTGGACCTACACCCGTCACGGGGCCACCCAG 694
 QY 105 HisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsn 124
 DB 695 CTGGCGAGGTCACCTCCGACGGCAGCGCTCTACGACATTTACCGCAGCGGCTCAAC 754
 QY 125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgAsnArg 144
 DB 755 CAGCCGTCCTCATCTCGGCACCGCCACCTTTACGAGTACTGGTCGTCGCGCCGCAACAC 814
 QY 145 ArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGlnGlyLeu 164
 DB 815 CGCTCGAGCGGCTCGTCAACACGCGGACCACTTCAAGCGTGGCTCAGCAAGGCTG 874
 QY 165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
 DB 875 ACGCTCGGACGATGATACAGATTGTTCCGCTGGAGGTTACTTTAGCTCTGGCTCT 934
 QY 185 AlaSerIleThrValSer 190
 DB 935 GCTTCCATACCCGTCAGC 952

RESULT 8

AAV29598

ID AAV29598 standard; DNA; 822 BP.

XX AC AAV29598;

XX DT 02-SEP-1998 (first entry)

XX DE DNA sequence of the specification.

XX KW Regulatory sequence; cellulase cbhl gene; mass production;

XX KM Humicola insolens; endo-glucanase NCE4; ds.

XX OS Trichoderma viride.

XX FH Key

XX FT CDS

XX FT 14. .812

XX FT /note= a

XX FT /tag= a

XX FT /note= "contains an intron"

XX FT sig_peptide

XX FT 14. .112

XX FT /tag= b

XX FT mat_peptide

XX FT 113. .809

XX FT /tag= c

XX FT intron

XX FT 286. .412

XX FT /tag= d

XX FT

XX PN W09811239-A1.

XX XX

XX PD 19-MAR-1998.

XX XX

XX PF 16-SEP-1997; 97WO-JP003268.

XX XX

XX PR 13-SEP-1996; 96JP-00243695.

XX XX

XX PA (MEIJ) MEIJI SEIKA KAISHA LTD.

XX XX

XX PI Watanabe M, Moriya T, Aoyagi K, Sumida N, Murakami T;

XX XX

XX DR WPI; 1998-250959/22.

XX DR P-PSDB; AAW57422.

XX XX

XX PT Regulatory sequence for Trichoderma viride derived cellulase cbhl gene -

XX PT for producing Humicola insolens derived endo-glucanase.

XX XX

XX PS Disclosure; Page 57-59; 92pp; Japanese.

XX XX

XX CC The present sequence appears in the specification. The specification

XX CC describes a new regulatory sequence for Trichoderma viride derived

CC cellulase cbhl gene and the establishment of a system for mass producing
 CC cellulase in moulds such as T. viride. As the regulatory sequence of cbhl
 CC genes originating in T. viride can highly express objective proteins,
 CC proteins such as cellulase can be expressed. An expression vector
 CC containing the regulatory sequence and Humicola insolens derived endo-
 CC glucanase NCE4 DNA was produced, and used to produce endo-glucanase at 15
 CC grams per litre

SQ Sequence 822 BP; 178 A; 280 C; 211 G; 153 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,64e-88 Length: 822

Score: 919.00 Matches: 176

Percent Similarity: 77.68% Conservative: 5

Best Local Similarity: 75.54% Mismatches: 9

Query Match: 87.86% Indels: 43

DB: 2 Gaps: 1

US-09-990-874B-55 (1-190) x AAV29598 (1-822)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20

DB 113 CAGACGATTTCAGCCGCGACGGCTACACACGGCTACTTCTACTCGTACTGGACGAC 172

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40

DB 173 GGCCACGGCGGCTGACGTACACCAATGGCCCGGGCCAGTTCTCCGTCACTGGTCC 232

QY 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrIys----- 56

DB 233 AACTCGGGCAACTTTGTTCGGCGCAGGGATGGCAGCCCGGCCACCAAGNACAAGTAAGAC 292

QY 56 ----- 56

DB 293 TATATACACCCCACTTCTGACCAAAACCCCTATCCACGACAGATATATAAACCAAGG 352

QY 57 -----AsnIys 58

DB 353 GCGTGATTATATGAGAGAGAGAGTGTGTGATCTAACGGTTTTTGTCTGAAACAAG 412

QY 59 -ValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGl 78

DB 413 GGTTCATCACTTCTCGGGCACCTACACCCCAACGCGCACAGCTTACCTCTCCGTGTACGG 472

QY 78 YTrpSerArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnPr 98

DB 473 CTGGTCGCGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCTACACCC 532

QY 98 oSerThrGlyAlaThrIysHisGlyGluValThrSerAspGlySerValTyrAspIleCy 118

DB 533 GTCCACCGCGCCCAACCAAGCTGGGAGGTGACGTCGACGGCAGCGCTCTACGACATCTA 592

QY 118 sArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTr 138

DB 593 CCGCAGCGAGCGGTCAACCCAGCGCTCATCGAGGCGCACCTCCACCTTTTACCAAGTACTG 652

QY 138 pSerValArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAl 158

DB 653 GTCGTCGCGCCGACCCACCGCTCCAGCGCTCCGTCACACGGCGAACCACTTCAACGC 712

QY 158 aTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGl 178

DB 713 GTGGGCTCGCAGCGCTGACGCTGGGCACCATGGATTACAGATTGTTGCCGTGGAGGG 772

QY 178 YTrpPheSerSerGlySerAlaSerIleThrValSer 190

DB 773 CTACTTTAGTCTGGGTCTGCTTCCATCCACCGTCAGC 809

XX

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xx 17-OCT-2003 (revised)
 DT 15-SEP-1997 (first entry)
 XX Chaetomium thermophilum xylanase A xlnA gene.
 DE Xylanase A; xlnA gene; pulp; bleaching; baking; ss.
 KW Chaetomium thermophilum; CBS 730.95 (ALKO4265).
 OS Chaetomium thermophilum; CBS 730.95 (ALKO4265).
 XX
 FH Key Location/Qualifiers
 FT exon 195..423
 FT sig_peptide 195..252
 FT intron 424..482
 FT exon 483..1039
 FT /*tag= c
 WO922692-A1.
 XX 26-JUN-1997.
 XX 17-DEC-1996; 96WO-FI000671.
 XX 18-DEC-1995; 95US-0008746P.
 PR 28-JUN-1996; 96US-0020839P.
 XX (PRIM-) PRIMALCO LTD.
 XX Paloheimo M, Hakola S, Maentylae A, Vehmaanperae J, Lantto R;
 PI Lehtinen T, Fagerstrom R, Suominen P;
 XX WPI; 1997-341683/31.
 DR P-PSDB; AAW18115.
 XX Nucleic acid encoding new xylanase(s) from Chaetomium thermophilum -
 PT useful for treating wood pulp, animal feed and flour, e.g. to facilitate
 PT bleaching.
 XX Claim 1; Page 42-43; 76pp; English.
 XX The Chaetomium thermophilum xlnA gene (AAT71585) codes for novel xylanase
 CC A (AAW18115), an enzyme that has a temperature optimum of over 50 deg C
 CC at pH 4-8 (partic. pH 5-7). Plasmid pALK1026 contg. the xlnA gene has
 CC been deposited as DSM 11021. The xlnA, xlnB (see also AAT71586) and xlnC
 CC (see also AAT71587) genes were isolated from a C. thermophilum CBS 730.95
 CC genomic library by hybridisation to the Trichoderma reesei xln2 gene. The
 CC isolated genes can be used for recombinant prodn. of C. thermophilum
 CC xylanases in transformed host cells (esp. T. reesei) for use in enzyme-
 CC aided bleaching of wood pulp and in methods of modifying plant biomass,
 CC e.g. as a feed additive or in baking. (Updated on 17-OCT-2003 to
 CC standardise OS field)
 XX Sequence 1281 BP; 308 A; 385 C; 324 G; 264 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 2.63e-63 Length: 1281
 Score: 687.00 Matches: 126
 Percent Similarity: 72.86% Conservative: 27
 Best Local Similarity: 60.00% Mismatches: 36
 Query Match: 65.68% Indels: 22
 DB: 2 Gaps: 2
 US-09-990-874b-55 (1-190) x AAT71585 (1-1281)
 Qy 1 GlnThrIle---GlnProGlyThrGlyThrHisAspGlyTyrPheTyrSerTyrTrpAsn 19
 Db 273 CAGACGCTCCACGACGAGTGCACCGGACCCCAATGCTGCTACTACAGCTTCTGGACC 332
 Qy 20 AspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrp 39

Db 333 GATGGCCAAAGGCAACATTCGCTTCAACCTCGAGAGCGGTGGCCAGTACAGCGTGACATGG 392
 Qy 40 SerAsnSerGlyAsnPheValGlyGlyLys- 49
 Db 393 TCTGGTAACGGCACTGGGTGGGGCAA-AGGTATGTCCTCTTTAAATGTTTCCAGCGCTA 451
 Qy 50 -----GlyTyrGlnProGlyThrLysAsnLysVal 59
 Db 452 TGGAAATGAACATAAATGCTAACTGTTAAACAGGCTGGAACCCCGGTACCGATAACCGTGC 511
 Qy 60 IleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrp 79
 Db 512 ATCACTACACGCGGACTACAGACCCACGCGCAACTCTACCTCGCGGCTACGCGTGG 571
 Qy 80 SerArgAsnProLeuIleGlyTyrTyrIleValGluAsnPheGlyThrTyrAsnProSer 99
 Db 572 ACCCGCAACCCGCTGATCGAGTACTAGTGTGCGAGGCTTCGGCACTTACGACCCGCTG 631
 Qy 100 ThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArg 119
 Db 632 ACGGGGCGCACCCGCTATGGCGAGTGTGAGAGCTTCGGCACTTACGACCCGCTG 691
 Qy 120 ThrGlnArgValAsnAlaProSerIleGlyGlyThrAlaThrPheTyrGlnTyrTrpSer 139
 Db 692 ACGCAGCGCTCAACGCGCCCTCCATCGAGGGCACCAAGACCTTCTACCAATACTGCT 751
 Qy 140 ValArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrp 159
 Db 752 GTGGCACCTCCAGCGCACCGCGGTACTGTTACCATGCGCAACCACTTCAATGCTGG 811
 Qy 160 AlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGlyTyr 179
 Db 812 AGGCAGCGTGTCTGCGAGCTGGGTTCCTCATGATATTCAGATTGTGGCTACTAGGAGTTAC 871
 Qy 180 PheSerSerGlySerAlaSerIleThrVal 189
 Db 872 TACTCGTCTGGCTCGCGCACTGTCAATGTT 901
 RESULT 10
 ABQ80364
 ID ABQ80364 standard; cDNA; 705 BP.
 AC ABQ80364;
 AC ABQ80364;
 DT 11-AUG-2003 (first entry)
 DE A. fumigatus AfXYL2 cDNA.
 KW Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
 KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
 KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
 KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
 KW glyceride; starch; maltodextrin; oxidized phenolic compound;
 KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
 KW textile; tea liquor; cleaning ability; ss.
 OS Aspergillus fumigatus.
 FH Key Location/Qualifiers
 FT CDS 1..705
 FT /*tag= a
 FT /product= "Xylanase 2"
 XX WO2003012071-A2.
 XX 13-FEB-2003.
 XX 05-AUG-2002; 2002WO-US024842.
 PR 03-AUG-2001; 2001US-0309870P.
 XX (ELIT-) ELITRA PHARM INC.
 XX

PI Jiang B, Storms R, Roemer T, Buseey H;
 DR WPI; 2003-332729/31.
 DR P-PSDB; ABB80186.
 XX
 PT Novel isolated *Aspergillus fumigatus* polypeptide, useful in various
 PT industries such as those involved in the making of food and feed,
 PT beverages, textiles and detergents.
 XX
 PS Claim 2; Page 165-66; 169pp; English.
 XX
 CC The sequences given in ABQ80319-66 encode enzymatic proteins derived from
 CC A. fumigatus. The resulting proteins display the catalytic activity of an
 CC enzyme such as tannase, cellulase, glucose oxidase, glucoamylase,
 CC phytase, beta-galactosidase, invertase, lipase, alpha-amylase, laccase,
 CC polygalacturonase or xylanase. Compositions comprising the tannase are
 CC useful for modulating the amount of compounds that comprise a gallate
 CC ester linkage in a composition. Compositions comprising cellulase are
 CC useful for modulating the amount of cellulose in a composition.
 CC Compositions comprising glucose oxidase are useful for modulating the
 CC amount of glucose or oxygen in a composition. Compositions comprising
 CC phytase are useful for modulating the amount of myo-inositol phosphates
 CC in a composition. Compositions comprising beta-galactosidase are useful
 CC for modulating the amount of lactose in a composition. Compositions
 CC comprising sucrose or invertase are useful for modulating the amount of
 CC sucrose in a composition. Compositions comprising lipase are useful for
 CC modulating the amount of glyceride in a composition. Compositions
 CC comprising alpha-amylase are useful for modulating the amount of
 CC starches or maltodextrins in a composition. Compositions comprising
 CC laccase are useful for modulating the amount of oxidized phenolic
 CC compounds in a composition. Compositions comprising polygalacturonase
 CC are useful for modulating the amount of high or low molecular weight
 CC polygalacturonic acid chains in a composition. Compositions comprising
 CC xylanase are useful for modulating the amount of xylan or xylo-oligomers
 CC in a composition. The A. fumigatus proteins and corresponding DNA's are
 CC useful in various industries such as those involved in the making of food
 CC and feed, beverages, textiles and detergents. The DNA's are useful to
 CC express recombinant enzymes for characterization, modification or
 CC industrial uses, to compare with the nucleotide sequence of A. fumigatus
 CC to identify duplicated genes of paralogs having the same or similar
 CC biochemical activity and/or function, to compare with nucleic acid
 CC sequence of other related or distant fungal organisms to identify
 CC potential orthologous enzyme genes, for selecting and making oligomers
 CC for attachment to a nucleic acid array for examination of expression
 CC patterns, and to raise anti-protein antibodies. The polypeptide having
 CC tannase activity increases the yield of tea liquor from tea leaves,
 CC improves the colour, flavour and health benefits of tea products,
 CC particularly an instant tea product. The polypeptide having cellulase
 CC activity enhances cleaning ability of detergent compositions
 XX
 SQ Sequence 705 BP; 151 A; 227 C; 183 G; 144 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3.01e-61 Length: 705
 Score: 664.50 Matches: 118
 Percent Similarity: 76.60% Conservative: 26
 Best Local Similarity: 62.77% Mismatches: 39
 Query Match: 63.53% Indels: 5
 DB: 10 Gaps: 1

US-09-990-874B-55 (1-190) x ABQ80364 (1-705)

Qy 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyGlyValThr 26
 Db 136 ACCGGCTGGACCAACGGCTACTACTCTCTGGACTGATGGCGGGCGACGTGACC 195
 Qy 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
 Db 196 TACACCAATGGCGCGGGTGGTTCCTCCGCTCACTGGAGAACGGTGGGCACTTTGTC 255
 Qy 47 GlyGlyLysGlyTyrGlnProGlyThrLys-----AsnLysValIleAsn 61
 Db 256 GGTGGAAAGGGCTGGAAACCTTGGAGAGCCCTAGGTAGTACCAGCTTTAAGTAGAACCATCAAC 315

Qy 62 PheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
 Db 316 TACGGAGCAGCTTCAACCCAGCGGCACATGGCTACTCTGGCTGTCTAGCGGTGGACACC 375
 Qy 82 AsnProLeuIleGlyTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGly 101
 Db 376 AACCCCTTGATTGAGTACTACGTTGTTGAGTCGTATGATACATACAAACCCCGGACGGC 435
 Qy 102 AlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspIleCysArgThrGln 121
 Db 436 GGTACCTTTCAGGGGCACTGTCAACACCGACGGTGGCACTTCAACAATCTACACGGCCGTT 495
 Qy 122 ArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArg 141
 Db 496 CGCTACATGCTCCCTCCATCGAAGGCCCAAGACCTTCCACCATGACTGTGTCTGTGGC 555
 Qy 142 ArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArg 161
 Db 556 ACCTCCAAGGCTACCGGGCGCACTGTCCACATGGCCCAACCACTTCAAGCCCTGGAGCAGA 615
 Qy 162 GlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSer 181
 Db 616 CTGGGCATGAACCTGGGAACCTCAACATACCAAGATTGTGGCACTGAGGGTTACAGAGC 675
 Qy 182 SerGlySerAlaSerIleThrVal 189
 Db 676 AGCGGATCTGCTTCATCATCTGTC 699
 XX
 RESULT 11
 ABQ80363
 ID ABQ80363 standard; DNA; 739 BP.
 AC ABQ80363;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DB A. fumigatus AfXYL2 DNA.
 XX
 KW Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
 KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
 KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
 KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
 KW glyceride; starch; maltodextrin; oxidized phenolic compound;
 KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
 XX textile; tea liquor; cleaning ability; ss.
 OS *Aspergillus fumigatus*.
 XX
 FN WO2003012071-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 05-AUG-2002; 2002WO-US024842.
 XX
 PR 03-AUG-2001; 2001US-0309870P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Jiang B, Storms R, Roemer T, Buseey H;
 XX
 DR WPI; 2003-332729/31.
 DR P-PSDB; ABB80186.
 XX
 PT Novel isolated *Aspergillus fumigatus* polypeptide, useful in various
 PT industries such as those involved in the making of food and feed,
 PT beverages, textiles and detergents.
 XX
 PS Disclosure; Page 164-65; 169pp; English.
 XX
 CC The sequences given in ABQ80319-66 encode enzymatic proteins derived from
 CC A. fumigatus. The resulting proteins display the catalytic activity of an
 CC enzyme such as tannase, cellulase, glucose oxidase, glucoamylase,

CC phytase, beta-galactosidases, invertase, lipase, alpha-amylase, laccase,
 CC polygalacturonase or xylanase. Compositions comprising the tannase are
 CC useful for modulating the amount of compounds that comprise a gallate
 CC ester linkage in a composition. Compositions comprising cellulase are
 CC useful for modulating the amount of cellulose in a composition.
 CC Compositions comprising glucose oxidase are useful for modulating the
 CC amount of glucose or oxygen in a composition. Compositions comprising
 CC phytase are useful for modulating the amount of myo-inositol phosphates
 CC in a composition. Compositions comprising beta-galactosidases are useful
 CC for modulating the amount of lactose in a composition. Compositions
 CC comprising sucrose or invertase are useful for modulating the amount of
 CC sucrose in a composition. Compositions comprising lipase are useful for
 CC modulating the amount of glyceride in a composition. Compositions
 CC comprising alpha-amylases are useful for modulating the amount of
 CC starches or maltodextrins in a composition. Compositions comprising
 CC laccase are useful for modulating the amount of oxidized phenolic
 CC compounds in a composition. Compositions comprising polygalacturonases
 CC are useful for modulating the amount of high or low molecular weight
 CC polygalacturonic acid chains in a composition. Compositions comprising
 CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
 CC in a composition. The A. fumigatus proteins and corresponding DNA's are
 CC useful in various industries such as those involved in the making of food
 CC and feed, beverages, textiles and detergents. The DNA's are useful to
 CC express recombinant enzymes for characterization, modification or
 CC industrial uses, to compare with the nucleotide sequence of A.fumigatus
 CC to identify duplicated genes of paralogs having the same or similar
 CC biochemical activity and/or function, to compare with nucleic acid
 CC sequence of other related or distant fungal organisms to identify
 CC potential orthologous enzyme genes, for selecting and making oligomers
 CC for attachment to a nucleic acid array for examination of expression
 CC patterns, and to raise anti-protein antibodies. The polypeptide having
 CC tannase activity increases the yield of tea liquor from tea leaves,
 CC improves the colour, flavour and health benefits of tea products,
 CC particularly an instant tea product. The polypeptide having cellulase
 CC activity enhances cleaning ability of detergent compositions
 XX

Sequence 739 BP; 158 A; 235 C; 195 G; 151 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,848-59 Length: 739
 Score: 648.00 Matches: 118
 Percent Similarity: 72.50% Conservative: 27
 Best Local Similarity: 59.00% Mismatches: 38
 Query Match: 61.95% Indels: 17
 DB: 10 Gaps: 1

US-09-990-874B-55 (1-190) x ABQ80363 (1-739)

QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
 DB 136 ACCGCTGGAAACACGGCTACTACTCTCTGGACTGATGGCGGCGGACGTGACC 195
 QY 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
 DB 196 TACACCAATGGCGCGGTGGCTCGTACTCCGTCACTGGAGGAACTGGGCAACTTTGTC 255
 QY 47 GlyGlyLysGlyTyrGlnProGlyThr----- 55
 DB 256 GGTGGAAGGGCTGGAAACCTCGAAGCGGTAGTACCGAGCTTTGTCACTGGATGTG 315
 QY 56 -----LysAsnLysValIleAsnPheSerGlySerTyrAsnProAsnG1 70
 DB 316 CAGACTGTGGCTGACAGAGTAGTACCACTACCTACGGAGGACGAGCTTCACCCAGCGG 375
 QY 70 YasnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIleGluTyrTrileVa 90
 DB 376 CAATGGCTACCTGGCTGTCTACGGCTGGACCAACCCCTTTGATTGAGTACTAGTTGT 435
 QY 90 IclAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSe 110
 DB 436 TGAGTCGTATGTATACATACACCCCGGACGCGCGGTACCTTCAGGGGCACTGTCAACAC 495
 QY 110 rAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGlu1 130

DB 496 CGACGGTGCACTTACAACTCTACACGCCGCTTGCCTACATGTCTCCTCATCGAAGG 555
 QY 130 YThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgArgSerSerGlySerVa 150
 DB 556 CACCAGACCTTCCACCGAGTACTGGTCTGTGGGCACTCCAAAGCTACCGGCGGCACTGT 615
 QY 150 lAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAs 170
 DB 616 CACCATGGCCAAACCACTTCAACGCCCTGGAGCAGACTGGGCACTGAACCTGGGAACCTCA 675
 QY 170 pTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThrVal 189
 DB 676 CTACCAGATTGTGGCCACTGAGGTTACCAAGCAGCAGCGGATCTGTCTCCATCACTGTTC 733
 RESULT 12
 AAS13813
 ID AAS13813 standard; DNA; 588 BP.
 AC AAS13813;
 DT 18-DEC-2001 (first entry)
 XX DNA encoding Thermomyces lanuginosus xylanase A.
 XX Xylanase A; plant cell wall; baking; cereal; starch production; wood;
 KW wood pulp bleaching; hemicellulose; arabinoxylan; foodstuff; bread; ds.
 XX Thermomyces lanuginosus.
 OS
 XX WO200166711-A1.
 XX 13-SEP-2001.
 XX 08-MAR-2001; 2001WO-IB000426.
 PR 08-MAR-2000; 2000GB-00005585.
 PR 27-JUN-2000; 2000GB-00015751.
 XX (DANI-) DANISCO AS.
 XX Sibbesen O, Sorensen JF;
 XX WPI; 2001-596834/67.
 PT Novel variant xylanase polypeptide or its fragment useful for degrading
 PT or modifying plant cell wall, comprises amino acid modifications such
 PT that the polypeptide has altered sensitivity to xylanase inhibitor.
 PS
 XX Disclosure; Page 64; 70pp; English.
 CC The invention relates to a variant xylanase polypeptide (I) or its
 CC fragment having xylanase activity, comprising one or more amino acid
 CC modifications such that (I) or its fragment has an altered sensitivity to
 CC a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or
 CC its coding sequence (II) is useful for degrading or modifying plant cell
 CC wall or for processing a plant material by contacting the plant cell wall
 CC or plant material with (I) or (II). (I) is useful for modifying plant
 CC materials, and in baking, processing cereals, starch production,
 CC processing wood and enhancing the bleaching of wood pulp. (I) is useful
 CC for altering the viscosity derived from the presence of hemicellulose or
 CC arabinoxylan in a solution or system comprising plant cell wall material.
 CC (I) is useful for preparing a foodstuff such as bread, pretzels,
 CC tortillas, cakes, cookies, biscuits or crackers. The present sequence
 CC represents the coding sequence of Thermomyces lanuginosus xylanase A as
 CC described in the method of the invention
 XX
 SQ Sequence 588 BP; 131 A; 178 C; 168 G; 111 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,12e-59 Length: 588
 Score: 643.50 Matches: 117
 Percent Similarity: 74.87% Conservative: 26

Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 5 Gaps: 1

US-09-990-874B-55 (1-190) x AAS13813 (1-588)

```
Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
Db 4 CAGACAAACCCCAACTCGAGGGCTGGCAGCATGGTATTACTATTCTCGTGGAGTGAC 63

Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 64 GGTGAGCGCAGCCAGCAGTACCACTGGAGCGGCAGCCTACGAGATCAGCTGGGGA 123

Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60
Db 124 GATGCGGTAACTCGTGGTGGAAAGGCTGGACCCCGGCTGACGCAAGACCATC 183

Qy 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
Db 184 CACTTTGAGGGTGTATTACAGCCAAACGCAACAGCTACTTGGCGTCTACGGTTGGACC 243

Qy 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
Db 244 CGCAACCCGCTGCTCGAGTATTACATCGTCGAGAACTTTGGCACCCTATGATCCTTCCTCC 303

Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
Db 304 GGTGCTACCGATCTAGGAACGTGCGAGTGGCAGCGTAGCATCTATCGACTCGGCAAGACC 363

Qy 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
Db 364 ACTCGCGTCAACGCACTAGCATCGACGCGCACCCCAACCTTCGACCAATCTCTGTCGCTC 423

Qy 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
Db 424 CGCCAGGACAAAGCGCACGCGGTATCGTCCAGACGGCGCTGCGCACTTCGACGCCCTGGGCT 483

Qy 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db 484 CGCGCTGTTTGAATGTCAACGGTGACCACTACTACCAAGATCGTTGGCAACGGAGGGCTAC 543

Qy 180 PheSerSerGlySerAlaSerIleThrValSer 190
Db 544 TTCAGCAGCGGTATGCTCGCATCACCGTGTCT 576
```

RESULT 13

AAD17927

AC AAD17927 standard; DNA; 678 BP.

AC AAD17927;

XX 10-DEC-2001 (first entry)

DT Thermomyces lanuginosus codon optimised xylanase gene.

DE Xylanase; Pichia cell; heterologous nucleotide; codon optimisation; ds.

XX Thermomyces lanuginosus.

XX Synthetic.

XX WO200166693-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-DK000154.

XX 10-MAR-2000; 2000DK-00000392.

XX 15-MAR-2000; 2000DK-00000419.

XX (NOVO) NOVOZYMES AS.

XX Takagi S, Terui Y, Teutsuni N, Taira R;

PI

XX WPI; 2001-582273/65.

XX Novel pichia cell useful for producing polypeptide of interest, comprises
PT a copy of heterologous nucleotide sequence encoding polypeptide of
PT interest.

XX Claim 14; Page 38-39; 61pp; English.

XX The invention relates to a Pichia cell comprising at least one copy of
CC heterologous nucleotide sequence encoding a polypeptide of interest,
CC where the codon usage of the sequence has been adjusted to match the
CC preferred codon usage of P. methanolica. The invention also relates to a
CC method for producing high yields of heterologous codon optimised
CC polypeptide in a Pichia cell. The Pichia cell is useful for producing a
CC polypeptide of interest, where the polypeptide is encoded by a nucleotide
CC sequence heterologous to P. methanolica. The present sequence is
CC Thermomyces lanuginosus codon optimised xylanase gene which is the
CC heterologous DNA used in the invention

XX SQ Sequence 678 BP; 180 A; 89 C; 152 G; 257 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.97e-59 Length: 678
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 4 Gaps: 1

US-09-990-874B-55 (1-190) x AAD17927 (1-678)

Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20

Db 94 CAAACAACCTCCAAATTCGAAGGTGGCATGATGTTATTATTATTCTTGGTGGCTCAT 153

Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40

Db 154 GGTGCTGCTCAAGCTACTTATCTAATAATTTAGAAGGTGGTACTATGAAATTTCTTGGGGT 213

Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60

Db 214 GATGGTGGTAAATTTAGTTGGTGGTAAAGGTGGAAATCCAGGTTTAAATGCAAGAGCTATT 273

Qy 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80

Db 274 CATTTTGAAGGTGTTTATCAACCAATGGTAAATCTTATTATTAGCTGTTTATGGTTGGACT 333

Qy 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100

Db 334 AGAAATCCATTTAGTTGAATATATATTGTTGAAAAATTTGGTACTTATGATCCATCTTCT 393

Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120

Db 394 GGTGCTACTGATTTAGGTACTGTTGAATGTGATGGTCTATTATTATAGATTAGGTAAATAA 453

Qy 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140

Db 454 ACTAGAGTTAATGACCAATCTATTGATGGTACTCAAACTTTCGATCATATATGGTCTGTT 513

Qy 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160

Db 514 AGACAAGATAAAAGAACTTCTGGTACTGTTCAAACCTGGTGTCAATTCGATGCTGGGCT 573

Qy 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179

Db 574 AGAGCTGGTTTGAATGTTAATGGTGGTCAATTTATTATCAAAATTTGTTGCAACGAGGTAT 633

Qy 180 PheSerSerGlySerAlaSerIleThrValSer 190

Db 634 TTCCTCTTCTGTTTATGCTAGAAATTACTGTGCT 666

RESULT 14

AAT40742
 ID AAT40742 standard; cDNA; 983 BP.
 XX
 AC AAT40742;
 XX
 DT 21-MAY-1997 (first entry)
 XX
 DE Xylanase coding sequence.
 XX
 KW Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermosascus;
 KW Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia;
 KW Byssoschlamus; Paecilomyces; animal feed additive; in-vivo breakdown;
 KW plant cell wall; growth rate; feed conversion; ss.
 XX
 OS Thermomyces lanuginosus.
 XX
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 31..708
 FT /*tag= a
 FT /product= "xylanase"
 XX
 FN WO9623062-A1.
 XX
 XX
 PD 01-AUG-1996.
 XX
 PF 26-JAN-1996; 96WO-DK000046.
 XX
 PR 26-JAN-1995; 95DK-00000094.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Hansen PK, Wagner P, Muellertz A, Knap IH;
 DR WPI; 1996-454790/45.
 DR P-PSDB; AAW01112.
 XX
 PT Fungal xylanase preps. for use as animal feed additives - and DNA
 PT construct for producing recombinant Thermomyces xylanase.
 PS Claim 5; Page 45-46; 69pp; English.
 CC This sequence represents the coding sequence for the xylanase from
 CC Thermomyces lanuginosus strain DSM 4109. The encoded xylanase, and
 CC xylanases derived from Humicola, Thermosascus, Chaetomium, Mucor,
 CC Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssoschlamus or
 CC Paecilomyces strains can be used in the monocomponent xylanase
 CC preparations of the invention. The xylanase preparations and the
 CC recombinant Thermomyces xylanase are useful as animal feed additives,
 CC which promote in-vivo breakdown of plant cell wall material and thus
 CC improve digestibility, growth rate and/or feed conversion
 XX
 SQ Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.1e-59 Length: 983
 Score: 643.50 Matches: 117
 Percent Similarity: 74.8% Conservative: 26
 Best Local Similarity: 61.26% Mismatches: 47
 Query Match: 61.52% Indels: 1
 DB: 2 Gaps: 1
 US-09-990-874B-55 (1-190) x AAT40742 (1-983)
 QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
 DB 124 CAGACAACCCCACTCGGAGGCTGGCAGCATGTTATTACTATCTCTGGTGGAGTGAC 183
 QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 DB 184 GGTGGAGGCGACGCCACCTGACCAACCTGGAGCGGCCTACGAGATCAGCTGGGA 243
 QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
 DB 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60

DB 244 GATGCGGTAACTCGTCGGTGGAAAGGGCTGGAAACCCCGCCCTGAACGCAAGACCCATC 303
 QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
 DB 304 CACTTTGAGGTGTTTACAGCCAAACGCAACAGCTACCTTGGGTCTACGGTTGGACC 363
 QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 364 CGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCCTATGATCCTTCTCTCC 423
 QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 424 GGTGCTACCGATCTAGGAACTGTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACC 483
 QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
 DB 484 ACTCGGTCACAGCCACCTAGCATCGAGCGGACCCCAACCTTCGACCAATATCTGGTCGGTC 543
 QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 DB 544 CGCCAGGACAAGCGCACCGCGGTACCGTCCAGAGCGGCTGCCACTTCGACGCTGGGCT 603
 QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
 DB 604 CGCGCTGGTTTGAATGTCAACGCGTGACCACTACTACAGATCGTTGCAACGAGGGGCTAC 663
 QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
 DB 664 TTCAGCAGCGGTATGCTCGCATCACCCTTGTCT 696
 RESULT 15
 AAT43010
 ID AAT43010 standard; cDNA; 983 BP.
 XX
 AC AAT43010;
 XX
 DT 16-OCT-2003 (revised)
 DT 22-FEB-1997 (first entry)
 XX
 DE Endo-1,4-beta-D-xylanase gene.
 XX
 KW Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;
 KW Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;
 XX flour; baking; dough; ss.
 OS Thermomyces lanuginosus; (strain DSM 4109).
 FH Key Location/Qualifiers
 FT 5'UTR 1..30
 FT /*tag= a
 FT CDS 31..708
 FT /*tag= b
 FT /product= "Endo-1,4-beta-D-xylanase"
 FT /note= "EC-3.2.1.8"
 FT 3'UTR 709..983
 FT /*tag= c
 XX
 XX
 FN WO9632472-A1.
 XX
 PD 17-OCT-1996.
 XX
 PF 11-APR-1996; 96WO-DK000171.
 XX
 PR 11-APR-1995; 95DK-00000435.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Jorgensen OB, Si JO, Jakobsen TS;
 XX
 DR WPI; 1996-477123/47.
 DR P-PSDB; AAW05187.
 XX
 PT Bread improving additive contg. xylanase from Thermomyces - and opt.

PT alpha-amylase, increases volume, improves anti-staling properties etc.
XX
PS
XX Claim 7; Page 30-31; 41pp; English.
XX
CC The sequence encodes an endo-1,4-beta-D-xylanase from *Thermomyces*
CC *lanuginosus* (*Humicola lanuginosa*), which may be used as a bread-
CC improving additive. The enzyme may be expressed recombinantly from a
CC plasmid pYES2.0 vector in *Saccharomyces cerevisiae* DSM 10133 (claimed),
CC and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour,
CC optionally along with other enzymes (amylase, maltogenase, lipase,
CC cellulase, hemicellulase, pentosanase, glucose-oxidase, lactase,
CC protease and/or peroxidase). The enzyme combines particularly well with
CC amylolytic enzymes, and may be used to improve baking properties of flour
CC and/or dough, by increasing volume and improving texture, flavour, crumb
CC softness, freshness and anti-staling properties, while improving dough
CC machinability and stability. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8, 1e-59 Length: 983
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 2 Gaps: 1

US-09-990-874B-55 (1-190) x AAT43010 (1-983)

QY 1 GlnThrIleGlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
DB 124 CAGACACCCCCCACTCGGAGGGCTGGCAGCATGGTTATTACTATCTCTGGTGGAGTGAC 183
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 184 GGTGGAGCGCAGGCGCAGGTACACCAACCTGGAGGCGGCACCTACGAGATCAGCTGGGGA 243
QY 41 AsnSerGlyAsnPheValGlyGlyValGlyTrpGlnProGlyThrLysAsnLysValIle 60
DB 244 GATCGCGGTAACTCGTCGGTGGAAAGGGCTGGAAACCCCGGCCCTGACGAGAGGCCATC 303
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 304 CACTTTGAGGGTGTATACACGCAACCGCAACAGCTACCTTGGCGTCTACGGTTGGACC 363
QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 364 CGCAACCGCTGTGTCGAGTATTACATCGTCGAGAACCTTGGCACCTATGATCTCTCTCC 423
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 424 GGTGCTACCGATCTAGGAACCTGTGAGTGGCAGCGTAGCATCTATCGACTCGGCAAGACC 483
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 484 ACTCGCTCAACGCACTAGCATCGACGCGCACCCCAACCTTGGACCAATACTGTCGCTC 543
QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 544 CGCCAGGACAAGCGCACCGGCTACCGTCCAGACGGGCTGCCACTTCGACGCTGGGCT 603
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 604 CGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAAGATCGTTGCAACGGAGGGCTAC 663
QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
DB 664 TTCAGCAGCGGCTATGTCTCGCATCACCGTTGCT 696

Search completed: December 30, 2005, 01:34:28
Job time : 480 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2005, 00:18:57 ; Search time 3753 Seconds
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2368.651 Million cell updates/sec

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Perfect score: 1046
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Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: gb_est7.*
9: gb_gsa1.*
10: gb_gsa2.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	932	89.1	744	7	CF867983
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3	877	83.8	768	7	CF881056
4	877	83.8	822	6	CB907827
5	680.5	65.1	738	6	CD464145
6	658.5	63.0	860	8	DR637934
7	658.5	63.0	883	8	DR643290

8	640.5	61.2	680	8	DR707969
9	640.5	61.2	746	8	DR701170
10	638	61.0	746	6	CB901964
11	638	61.0	746	7	CF871731
12	629.5	60.2	664	8	DR705641
13	623.5	59.6	682	8	DR702584
14	623	59.6	750	9	AQ160254
15	622.5	59.5	712	7	CV496238
16	616	58.9	743	7	CF865758
17	616	58.9	802	6	CB895680
18	609.5	58.3	772	7	CN133022
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20	608.5	58.2	639	8	DR624928
21	608.5	58.2	686	8	DR624738
22	608.5	58.2	719	8	DR631520
23	608.5	58.2	733	8	DR630899
24	608.5	58.2	739	8	DR624376
25	608.5	58.2	749	8	DR623097
26	608.5	58.2	763	8	DR624330
27	608.5	58.2	784	8	DR628641
28	608.5	58.2	801	8	DR631291
29	608.5	58.2	807	8	DR621776
30	608.5	58.2	809	8	DR627394
31	608.5	58.2	842	8	DR630275
32	608.5	58.2	886	8	DR621753
33	608.5	58.2	891	8	DR632055
34	608.5	58.2	916	8	DR622008
35	606.5	58.0	729	8	DR629975
36	606.5	58.0	763	8	DR623625
37	602.5	57.6	741	8	DR625790
38	600.5	57.4	882	8	DR037502
39	593.5	56.7	708	8	DR631672
40	591.5	56.5	675	8	DN588726
41	589.5	56.4	670	8	DR701228
42	589.5	56.4	711	8	DR622988
43	589.5	56.4	770	8	DR622508
44	582.5	55.7	627	8	DR702024
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ALIGNMENTS

RESULT 1

CF867983 LOCUS 744 bp mRNA linear EST 31-OCT-2003
DEFINITION tricol3xe09.b1 T.reesei mycelial culture, Version 6 October 2003
ACCESSION CF867983
KEYWORDS EST.
SOURCE CF867983.1 GI:38122635
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)
REFERENCE 1 (bases 1 to 744)
AUTHORS Rukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D., Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K., Ward, M. and Dean, R.A.

Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from Trichoderma reesei

JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)

PUBMED 14757250

COMMENT

Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: Tr-F1 primer.
Location/Qualifiers
source 1. .744


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/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
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/clone_lib="T. reesei mycelial culture, Version 6 October 2003"
/notes="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

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Pred. No.: 6,63e-95 Length: 744
Score: 932.00 Matches: 173
Percent Similarity: 95.16% Conservativeness: 4
Best Local Similarity: 93.01% Mismatches: 8
Query Match: 89.10% Indels: 1
DB: 7 Gaps: 0

US-09-990-874B-55 (1-190) x CF867983 (1-744)
Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
Db 185 CAGACGATTTCAGCGCGGCACGGGCTACAAACACGGCTACTTCTACTCGTACTGGAAACGAT 244
Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 245 GGCACCGCGCGGCTGACGTACCAATGCTCCCGCGGCGAGTTCCTCGTCAACTGGGTCC 304
Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60
Db 305 AACTCGGCAACTTGTTCGGCGGAGGATGGCGAGCGCGGACCAACAGAGTCAATC 364
Qy 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
Db 365 AACTTCTCGGCGAGCTACAAACCCCAACGCAACAGTACTCTCCGTGTACGGTGGTCC 424
Qy 81 ArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
Db 425 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCCTACAAACCGTCCAG 484
Qy 101 GlyAlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspIleCysArgThr 120
Db 485 GCGCCACCAAGCTCGGCGAGTCACTCCGACGCGGAGGCTACGACATTTACCGCAGC 544
Qy 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
Db 545 CAGCGCGTCAACACGCGCTCCATCATCGGCACCGCCACCTTTTACAGTACTGGTCCGTC 604
Qy 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
Db 605 CGCCGCAACACCGCTCGAGCGGCTCCGTCACACGCGGCAACCACTTCAACCGCGGGCT 664
Qy 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaVal-GluGlyTyrPh 180
Db 665 CAGCAGGCGCTGACGCTCGGGAGATGATGATGATGATGATGATGATGATGATGATGAT 724
Qy 180 eSerSerGlySerAla 185
Db 725 TAGCTCTGGCTCTGCT 740

RESULT 2
LOCUS CB898036
DEFINITION tricolix09 T. reesei mycelial culture, Version 3 april Hypocrea jecorina cDNA clone tricolix09, mRNA sequence.
ACCESSION CB898036
VERSION CB898036.1 GI:30112694
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina

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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 799)
Foreman, P.K., Brown, D.B., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
12788920
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
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/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tricolix09"
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/clone_lib="T. reesei mycelial culture, Version 3 april"
/notes="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN
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Pred. No.: 7,3e-95 Length: 799
Score: 932.00 Matches: 173
Percent Similarity: 95.16% Conservativeness: 4
Best Local Similarity: 93.01% Mismatches: 8
Query Match: 89.10% Indels: 1
DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x CB898036 (1-799)
Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
Db 240 CAGACGATTTCAGCGCGGCACGGGCTACAAACACGGCTACTTCTACTCGTACTGGAAACGAT 299
Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 300 GGCACCGCGCGGCTGACGTACCAATGCTCCCGCGGCGAGTTCCTCGTCAACTGGTCC 359
Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60
Db 360 AACTCGGCAACTTGTTCGGCGGAGGATGGCGAGCGCGGACCAACAGAGTCAATC 419
Qy 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
Db 420 AACTTCTCGGCGAGCTACAAACCCCAACGCAACAGTACTCTCCGTGTACGGTGGTCC 479
Qy 81 ArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
Db 480 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCCTACAAACCGTCCAG 539
Qy 101 GlyAlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspIleCysArgThr 120
Db 540 GCGCCACCAAGCTCGGCGAGGCTACCTCCGACGCGGAGGCTACGACATTTACCGCAGC 599
Qy 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
Db 600 CAGCGCGTCAACACGCGCTCCATCATCGGCACCGCACCTTTTACAGTACTGGTCCGTC 659
Qy 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
Db 660 CGCCGCAACACCGCTCGAGCGGCTCCGTCACACGCGGCAACCACTTCAACCGCGGGCT 719

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Qy 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaVal-GluGlyTyrPhe 180
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Qy 180 eSerSerGlySerAla 185
 Db 780 TAGCTCTGGCTCTGCT 795

RESULT 3
 CF881056 768 bp mRNA linear EST 31-OCT-2003
 LOCUS trico83xj11.b1 T.reesei mycelial culture, Version 6 October 2003
 DEFINITION Hypocrea jecorina cDNA clone trico83xj11. mRNA sequence.
 ACCESSION CF881056
 VERSION CF881056.1 GI:38135738
 KEYWORDS EST.
 SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
 ORGANISM Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 REFERENCE 1 (bases 1 to 768)
 AUTHORS Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
 Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
 Ward,M. and Dean,R.A.
 TITLE Characterization of the protein processing and secretion pathways
 in a comprehensive set of expressed sequence tags from Trichoderma
 reesei
 JOURNAL FEWS Microbiol. Lett. 230 (2), 275-282 (2004)
 PUBMED 14757250
 COMMENT Contact: Ralph A. Dean
 Fungal Genomics Laboratory
 North Carolina State University
 Campus Box 7251, Raleigh, NC 27695, USA
 Tel: 919-513-0020
 Fax: 919-513-0024
 Email: ralph.dean@ncsu.edu
 Seq primer: LT-F1 primer.
 Location/Qualifiers

FEATURES
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 /mol_type="mRNA"
 /strain="QM6a"
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 /clone="trico83xj11"
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 /clone_libs="T.reesei mycelial culture, Version 6 October 2003"
 /note="Vector: pREP3y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN
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 Pred. No.: 1.19e-88 Length: 768
 Score: 877.00 Matches: 167
 Percent Similarity: 90.00% Conservative: 4
 Best Local Similarity: 87.89% Mismatches: 19
 Query Match: 83.84% Indels: 1
 DB: 7 Gaps: 0

US-09-990-874B-55 (1-190) x CF881056 (1-768)

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 Db 189 CAGACGATTACGCCCGGACCGGCTACACACGCGCTACTTCTACTCGTACTGGAACGAT 248

Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 Db 249 GGCACACGCGCGGTGACGTACACCAATGCTCCGCGGCGGCGAGTTCTCCGTCAACTGGTCC 308

Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60

Db 309 AACTCGGCGCAACTTGTTCGGCGGCAAGGATGGCAGCCGCCGACCAAGACAGGTCAATC 368

Qy 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
 Db 369 AACTTCTCGGCGAGCTACACCCCAACGCGCAACAGTACCTCTCCGTGTACGGTGGTCC 428

Qy 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 Db 429 CGCAACCCCTGATCGAGTACTACATCGTTCGAGAACCTTGGCACCTACACCCGCTCCAG 488

Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
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Qy 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
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Qy 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 Db 668 CAGCAAGGCGCTGACGCTCGNACGATGGATACCAGATGTTGCCGTGGAGGGTACTTNT 727

Qy 181 SerSerGlySerAlaSerIleThrValSer 190
 Db 728 AGCTCTGGCTCTGCTTCCATCACCCTGTCAGC 757

RESULT 4
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 LOCUS trico83xj11 T.reesei mycelial culture, Version 3 april Hypocrea
 DEFINITION jecorina cDNA clone trico83xj11, mRNA sequence.
 ACCESSION CB907827
 VERSION CB907827.1 GI:30122485
 KEYWORDS EST.
 SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
 ORGANISM Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 REFERENCE 1 (bases 1 to 822)
 AUTHORS Foreman,P.K., Brown,D.B., Dankmeyer,L., Dean,R., Diener,S.,
 Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
 Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
 Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
 TITLE Transcriptional regulation of biomass-degrading enzymes in the
 filamentous fungus Trichoderma reesei
 JOURNAL J. Biol. Chem. 278 (34), 31988-31997 (2003)
 PUBMED 12788920
 COMMENT Contact: Pamela K. Foreman
 Genencor Intl.
 925 Page Mill Road, Palo Alto, CA 94304, USA
 Tel: (650) 846-7635
 Fax: (650) 621-7817
 Email: Pforeman@genencor.com
 Seq primer: LT-F1 primer.
 Location/Qualifiers

FEATURES
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 /organism="Hypocrea jecorina"
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 /note="Vector: pREP3y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

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Pred. No.: 1.3e-88 Length: 822
 Score: 877.00 Matches: 167
 Percent Similarity: 90.00% Conservativeness: 4
 Best Local Similarity: 87.89% Mismatches: 19
 Query Match: 83.84% Indels: 1
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x CB907827 (1-822)

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QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 DB 303 GCCACACGGCGGTGACGTACACCAATGGTCCGGGGGACGTTCTCCGTCACTGGTCC 362

QY 41 AsnSerGlyAsnPheValGlyGlyGlyTyrGlnProGlyThrLysAsnLysValIle 60
 DB 363 AACTCGGGCAACTTGTTCGGCGCAAGGATGGCAGCCGCGGACCAAGCAAGGTCATC 422

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
 DB 423 AACTTCTCGGGCAGCTACAACCCCAACGCAACAGCTACCTCTCCGTGTACGGCTGGTCC 482

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 483 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCAGCTACCAACCCGTCACG 542

QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 543 GGGCGCACCAAGCTGGCGGAGGTCACTCCGACGGCAGGCTCTACGACATTTACCGCAGC 602

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 DB 603 CAGCGCGTCAACACGCGTCCATCATCGGCACCGNCACCTTNTACGAGTACTGGTCCGTTN 662

QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 DB 663 NCGCCCAACCCCGTTCGAGCGGGCTCGTCTAC-ACGGGNAACATTTCAACCGTGGGCT 721

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 722 CAGCAAGCGCTGACGCTCGNGACGATGGATTACCCAGATGTTTGGCGTGAGGGTACTNT 781

QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 782 AGCTCTGGCTCTGCTTCCATCACCGCTCAGC 811

RESULT 5
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 LOCUS ETH1_48_B06.g1_A002 Ethylene-treated seedlings Sorghum bicolor cDNA
 DEFINITION clone ETH1_48_B06_A002 5', mRNA sequence.

ACCESSION CD464145
 VERSION CD464145.1 GI:31385413
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 738)
 Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,
 Klein,R.R., Lian,C., Sun,F., Sullivan,R., Shah,M., Salzman,R.,
 Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P.,
 Olaseinde,O., Eastman,A. and Pratt,L.H.
 An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
 (ACC)-treated seedlings
 Unpublished (2003)
 Other ESTs: ETH1_48_B06.b1_A002
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; plant material and RNA prepared at Texas A & M University;
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below Phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).
 Location/Qualifiers
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 /clone_lib="Ethylene-treated seedlings"
 /note="Vector: pME18S-FL3; Site_1: XhoI; Site_2: XhoI; The
 library was prepared from polyA+ RNA from seedlings grown
 in hydroponic culture. At 8 days of age, medium was
 supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
 acid (ACC) to induce endogenous ethylene (ETH) production.
 Roots and shoots were harvested after 27 and 72 hr and
 material from both time points was combined prior to RNA
 isolation. Double-stranded cDNA was cloned
 unidirectionally into different DraIII sites of the
 pME18S-FL3 vector (5'-prime DraIII site is CACTGTGTG,
 3'-prime DraIII site is CACCATGTG). XhoI excises the cDNA
 insert."

ORIGIN

Alignment Scores:
 Pred. No.: 2.11e-66 Length: 738
 Score: 680.50 Matches: 126
 Percent Similarity: 77.96% Conservativeness: 19
 Best Local Similarity: 67.74% Mismatches: 40
 Query Match: 65.06% Indels: 1
 DB: 6 Gaps: 1

US-09-990-874B-55 (1-190) x CD464145 (1-738)

QY 4 GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGly 23
 DB 182 CAGCCCACTACTGGCTCAAGCGGTGGTACTACTCTCTCTTCTGACTGATACACCCCAAC 241

QY 24 GlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGly 43
 DB 242 TCTGTCACTTACACCAACGCGGACCGTTCAGCTGCACTGCAATGGAACGAT 301

QY 44 AsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSer 63
 DB 302 AACCAAGTCTGGTGGAAAGGCTGGATGCCGCTGGTGTCT---CGCACCATCAAGTACTCT 358

QY 64 GlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnPro 83
 DB 359 GGTACTTACAACATCAACCGAAACAGCTACCTCGCTGTTTACGGATGGACTCAGAACCCCT 418

QY 84 LeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103
 DB 419 CTCATCGAGTACTACATCGTTGAGAACTTCGGCACTCAACCCCTCTTCCGGCGGCCGAG 478

QY 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123
 DB 479 AAGAGGGTGGAGTCACTGTTGACGGATCTCTACGACATCTACGTGACGACCCGCTGTC 538

QY 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsn 143


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/clone="FVWCX47"
/tissue_type="mycelia"
/clone_lib="FVM"
/note="Vector: pBluescript II SK(+) XR, Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FVM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN
Alignment Scores:
Pred. No.: 8,396-64 Length: 883
Score: 658.50 Matches: 116
Percent Similarity: 78.26% Conservative: 28
Best Local Similarity: 63.04% Mismatches: 39
Query Match: 62.95% Indels: 1
DB: 8 Gaps: 1

US-09-990-874B-55 (1-190) x DR643290 (1-883)

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Db 136 TCCGGTACTAACACGAGATTCTTCTACTCCGTGGAGTGATGGCGGTGCGCATGCTACT 195
Qy 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTTPSerAsnSerGlyAsnPheVal 46
Db 196 TACACCAACGCTGAGGAGGTCTTACTCCATGGAGTGGAGGATGGTGTAACTGCTC 255
Qy 47 GlyGlyLysGlyTTPGlnProGlyThrLysAsnLysValLleAsnPheSerGlySerTyr 66
Db 256 GGTGGTAAAGGTTGGTCTCTCGA---AAAGCTCGAACCATTCTCTATGAGGAGAGTAC 312
Qy 67 AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTTPSerArgAsnProLeuLleGlu 86
Db 313 AAGCCCAACGGCAACAGACTACTCTCGTCTACGGCTGAGACCCGAAACCCCTAGTCGAG 372
Qy 87 TyrTrileValGluAsnPheGlyThrTyrAsnProSerThrGlyValAlaThrLysHisGly 106
Db 373 TACTACATCTGATGAGTCTCTCGTACCTACACCCCTCCAGCGGTGCTACCAAGAGGT 432
Qy 107 GluValThrSerAspGlySerValTyrAspLecysArgThrGlnArgValAsnAlaPro 126
Db 433 ACCGTTGAGGCTGATGGCAGCACCTACGACATCTTCGAGACTACTCGCACCAACGCCCT 492
Qy 127 SerileGluGlyThrAlaThrPheTyrGlnTyrTTPSerValArgAsnArgSer 146
Db 493 TCAATCGACGGTACTCAGACCTTCAGCAGTACTGGTCTGTTCCGCGCAGCAGCATCGCT 552
Qy 147 SerGlySerValAsnThrAlaAsnHisPheAsnAlaTTPAlaArgGlnGlyLeuThrLeu 166
Db 553 ACTGTAGCGTTGACACTGGTCTTCCTTCAGCGCTGGAGAACGGCTGTATGAGTCT 612
Qy 167 GlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
Db 613 GGTACCCACGACTACCATCTCTGCTACTGAGGTTACTTTCAGCAGCGGATCTTCTCAC 672
Qy 187 IleThrValSer 190
Db 673 ATGACCGTTTCT 684

RESULT 8
LOCUS DR707969 680 bp mRNA linear EST 14-JUL-2005
DEFINITION Asn_08783 Aspergillus niger pBluescript (EcoRI-XhoI) Aspergillus
niger cDNA clone Asn_08783, mRNA sequence.
ACCESSION DR707969
VERSION DR707969.1 GI:70824260

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KEYWORDS EST.
SOURCE Aspergillus niger
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 680)
AUTHORS Tsang,A., Storms,R. and Bulter,G.
TITLE Expressed sequence tags from Aspergillus niger cDNA library
JOURNAL Unpublished (2005)
COMMENT Contact: Tsang A
Centre for Structural and Functional Genomics
Concordia University
7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada
Tel: 514 848 2424 3405
Fax: 514 848 4504
Email: tsang@vax2.concordia.ca
POLYA=No.

FEATURES
Location/Qualifiers
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/clone="Asn_08783"
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/lab_host="E. coli"
/clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
/note="Vector: pBluescript KS+; Site 1: XhoI; Site 2:
EcoRI; Complementary DNA was synthesized with ZAP Kit
(Stratagene) using poly(A)+RNA isolated from Aspergillus
niger cultured under different carbon sources (glucose,
maltose, xylose, lactose, sorbitol, xylan, and bran).
Synthesis was primed with oligo(dT)/XhoI primer. EcoRI
adaptors were ligated to the blunt-ended, double-stranded
cDNA. The EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp)."

ORIGIN
Alignment Scores:
Pred. No.: 6,478-62 Length: 680
Score: 640.50 Matches: 115
Percent Similarity: 77.60% Conservative: 27
Best Local Similarity: 62.84% Mismatches: 40
Query Match: 61.23% Indels: 1
DB: 8 Gaps: 1

US-09-990-874B-55 (1-190) x DR707969 (1-680)

Qy 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTTPAsnAspGlyHisGlyValThr 26
Db 10 ACCGGCGAGAACACGGCTTCTACTCTCTCTGGACCGCGGGTGGAGACGTGACC 69
Qy 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTTPSerAsnSerGlyAsnPheVal 46
Db 70 TACACCAACGAGATGCTGGTGGCTTACACTCTGAGTGGTCCACGCTGGGCACTTTGTC 129
Qy 47 GlyGlyLysGlyTTPGlnProGlyThrLysAsnLysValLleAsnPheSerGlySerTyr 66
Db 130 GGTGGAAGGGCTGGAACCCCGAAGTGGCGGAGAC---ATCACCTACAGCGGCACCTTC 186
Qy 67 AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTTPSerArgAsnProLeuLleGlu 86
Db 187 ACCCTTAGCGCAACGGCTACTCTCCGTCTATGGTGGACCACTGACCCCTCTGATCGAG 246
Qy 87 TyrTrileValGluAsnPheGlyThrTyrAsnProSerThrGlyValAlaThrLysHisGly 106
Db 247 TACTACATCTGTCGAGTCTCTACGCGACTTACACCCCGCGAGTGGAGGCGACGTACAAGGC 306
Qy 107 GluValThrSerAspGlySerValTyrAspLecysArgThrGlnArgValAsnAlaPro 126
Db 307 ACCCTACCTCGGACGGATCCGTTTACGATATCTACCGGTACCCGTACCACTCTCTCT 366
Qy 127 SerileGluGlyThrAlaThrPheTyrGlnTyrTTPSerValArgAsnArgSer 146

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Db 367 TCCATTGAGGAACCGCTACCTTCACTCAGTACTGGTCCGTTCCGCGCAGAACCAAGAGAGTT 426
Qy 147 SerGlySerValAsnThrAlaAsnHisPheAsnAlaThrAlaArgGlnGlyLeuThrLeu 166
Db 427 GCGGGAACCGTTACCACTCCCAACACCTTCAATGCTGGGCTTAAGCTGGGAATGAACCTG 486
Qy 167 GlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
Db 487 GGTACTCAACTACCAATGCTGGCTACCGAGGGTTACCAAGAGCGTGGATCTTCGTCC 546
Qy 187 IleThrVal 189
Db 547 ATCACTGTT 555

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RESULT 9
DR701170 746 bp mRNA linear EST 14-JUL-2005
LOCUS Asn_00615 Aspergillus niger pBluescript (EcoRI-XhoI) Aspergillus
DEFINITION niger cDNA clone Asn_00615, mRNA sequence.
ACCESSION DR701170
VERSION DR701170.1 GI:70817461
KEYWORDS EST.
SOURCE Aspergillus niger
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 746)
Tsang,A., Storms,R. and Bulter,G.
Expressed sequence tags from Aspergillus niger cDNA library
Unpublished (2005)
Contact: Tsang A
Centre for Structural and Functional Genomics
Concordia University
7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada
Tel: 514 848 2424 3405
Fax: 514 848 4504
Email: tsang@vax2.concordia.ca
POLYA=No.
Location/Qualifiers
1..746
/organism="Aspergillus niger"
/mol_type="mRNA"
/strain="N402"
/db_xref="taxon:5061"
/clone="Asn_00615"
/dev_stages="mycelial growth"
/lab_host="E. coli"
/clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
EcoRI; Vector: pBluescript KS+; Site 1: XhoI; Site 2:
(Stratagene) using poly(A)+RNA isolated from Aspergillus
niger cultured under different carbon sources (glucose,
maltose, xylose, lactose, sorbitol, xylan, and bran).
Synthesis was primed with oligo(dT)/XhoI primer. EcoRI
adaptors were ligated to the blunt-ended, double-stranded
cDNA. The EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp).

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FEATURES

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/dev_stages="mycelial growth"
/lab_host="E. coli"
/clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
EcoRI; Vector: pBluescript KS+; Site 1: XhoI; Site 2:
(Stratagene) using poly(A)+RNA isolated from Aspergillus
niger cultured under different carbon sources (glucose,
maltose, xylose, lactose, sorbitol, xylan, and bran).
Synthesis was primed with oligo(dT)/XhoI primer. EcoRI
adaptors were ligated to the blunt-ended, double-stranded
cDNA. The EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp).

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ORIGIN

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Alignment Scores:
Pred. No.: 7,34e-62 Length: 746
Score: 640.50 Matches: 115
Conservative: 77.60%
Best Local Similarity: 62.84%
Query Match: 61.23%
DB: 8 Gaps: 1

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US-09-990-874B-55 (1-190) x DR701170 (1-746)

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Qy 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
Db 149 ACCGCGGAGAACACGGCTTCTACTACTCTTCTGACCGCGGTGGAGACGTGACC 208

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Qy 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
Db 209 TACACCAACGAGAGTGTGGTGCCTCAGTGTTCAGTGGTCCACACGCTGGGCACTTTGTC 268
Qy 47 GlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSerGlySerTyr 66
Db 269 GGTGGAAAGGGCTGGAAACCCCGGAAGTGGCGAGAC---ATCACCTACAGCGGACCTTC 325
Qy 67 AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrPheSerArgAsnProLeuIleGlu 86
Db 326 ACCCTAGCGGCAACGGCTACTCTCGGTCTATGGTGGACCACTGACCCCTCTGATCGAG 385
Qy 87 TyrTrileValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGly 106
Db 386 TACTACATCGTTCGAGTCTCTACGGCGACTACCAACCCCGCGAGTGGAGGACGCTACAGGGC 445
Qy 107 GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
Db 446 ACCGTCACTCCGAGCGGATCCGTTTACGATATCTACACGGTACCCGTACCCATGCTGCT 505
Qy 127 SerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSer 146
Db 506 TCCATTAGGGAACCGTACTCTTCACTCAGTACTGGTCCGTTGCGCAGACCAAGAGAGTT 565
Qy 147 SerGlySerValAsnThrAlaAsnHisPheAsnAlaThrAlaArgGlnGlyLeuThrLeu 166
Db 566 GCGGGAACCGTTACCACTCCCAACCACTTCAATGCTTGGGCTAAGCTGGGAATGAACCTG 625
Qy 167 GlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
Db 626 GGTACTCACACTACCAATGCTGGCTACCGAGGGTTACCAAGAGCGTGGATCTTCGTCC 685
Qy 187 IleThrVal 189
Db 686 ATCACTGTT 694

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RESULT 10

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CB901964 746 bp mRNA linear EST 02-JUL-2003
LOCUS trico28x108 T. reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone trico28x108, mRNA sequence.
ACCESSION CB901964
VERSION CB901964.1 GI:30116622
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 746)
Foreman,P.K., Brown,D.B., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
12788920
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
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/organism="Hypocrea jecorina"
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/strain="QM6a"
/db_xref="taxon:51453"
/clone="trico28x108"
/dev_stages="mycelia"

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/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN
Alignment Scores:
Pred. No.: 1,41e-61 Length: 746
Score: 638.00 Matches: 122
Percent Similarity: 82.24% Conservative: 3
Best Local Similarity: 80.26% Mismatches: 27
Query Match: 60.99% Indels: 0
DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x CB901964 (1-746)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAep 20
|||||
DB 291 CAGACGANNACGCCGCGCAGCTACACACCCGCTACNNCTACTCGNACCGGAACGAN 350

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
|||||
DB 351 GGCCAAAAGCGGACGACGACCAAGGNCNCCGCGGCGAGNCTTCGCCCAACCGGGGCC 410

QY 41 AenSerGlyAsnPhaValGlyGlyGlyTyrGlnProGlyThrLysAenLysValIle 60
|||||
DB 411 AACNCGGGCAACNNGNCGCGGCGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 470

QY 61 AenPheSerGlySerTyrAsnProAenGlyAenSerTyrLeuAlaValTyrGlyTrpSer 80
|||||
DB 471 AACTTCTCGGCGAGCTACACCCCAACGCGCAACAGCTACTCTCGGTGTACGGGTGGTCC 530

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAenPheGlyThrTyrAsnProSerThr 100
|||||
DB 531 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCTTACCAACCCGCTCCAG 590

QY 101 GlyAlaThrLysHisGlyValThrSerAspGlySerValTyrAspIleCysArgThr 120
|||||
DB 591 GCGGCGCACCACTGGCGAGGTCACTCCGACGGGAGGCTACGACATTTACCGCAGC 650

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
|||||
DB 651 CAGCGCGTCAACACGCGCTCATCGGCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGTC 710

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThr 152
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DB 711 CGCGCGACCCACCGCTCGAGCGGGTCCGTCAACACG 746

RESULT 11
CF871731
LOCUS trico28xi08.b1 T.reesei mycelial culture, Version 6 October 2003 EST 31-OCT-2003
DEFINITION Hypocrea jecorina cDNA clone trico28xi08, mRNA sequence.
ACCESSION CF871731
VERSION CF871731.1 GI:38126413
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
REFERENCE 1 (bases 1 to 746)
AUTHORS Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
TITLE Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei
JOURNAL FEWS Microbiol. Lett. 230 (2), 275-282 (2004)
PUBMED 14757250
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: IT-F1 primer:
Location/Qualifiers
1..746

FEATURES
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/mol_type="mRNA"
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/clone_lib="T.reesei mycelial culture, Version 6 October
2003"
/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN
Alignment Scores:
Pred. No.: 1,41e-61 Length: 746
Score: 638.00 Matches: 122
Percent Similarity: 82.24% Conservative: 3
Best Local Similarity: 80.26% Mismatches: 27
Query Match: 60.99% Indels: 0
DB: 7 Gaps: 0

US-09-990-874B-55 (1-190) x CF871731 (1-746)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAep 20
|||||
DB 291 CAGACGANNACGCCGCGCAGCTACACACCCGCTACNNCTACTCGNACCGGAACGAN 350

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
|||||
DB 351 GGCCAAAAGCGGACGACGACCAAGGNCNCCGCGGCGAGNCTTCGCCCAACCGGGGCC 410

QY 41 AenSerGlyAsnPhaValGlyGlyGlyTyrGlnProGlyThrLysAenLysValIle 60
|||||
DB 411 AACNCGGGCAACNNGNCGCGGCGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 470

QY 61 AenPheSerGlySerTyrAsnProAenGlyAenSerTyrLeuAlaValTyrGlyTrpSer 80
|||||
DB 471 AACTTCTCGGCGAGCTACACCCCAACGCGCAACAGCTACTCTCGGTGTACGGGTGGTCC 530

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAenPheGlyThrTyrAsnProSerThr 100
|||||
DB 531 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCTTACCAACCCGCTCCAG 590

QY 101 GlyAlaThrLysHisGlyValThrSerAspGlySerValTyrAspIleCysArgThr 120
|||||
DB 591 GCGGCGCACCACTGGCGAGGTCACTCCGACGGGAGGCTACGACATTTACCGCAGC 650

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
|||||
DB 651 CAGCGCGTCAACACGCGCTCATCGGCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGTC 710

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThr 152
|||||
DB 711 CGCGCGACCCACCGCTCGAGCGGGTCCGTCAACACG 746

RESULT 12
DR705641
LOCUS Asn_05863 Aspergillus niger mRNA linear EST 14-JUL-2005
DEFINITION Asn_05863 Aspergillus niger cDNA clone Asn_05863, mRNA sequence.
ACCESSION DR705641
VERSION DR705641.1 GI:70821932
KEYWORDS EST.
SOURCE Aspergillus niger
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.


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REFERENCE 1 (bases 1 to 664)
AUTHORS Tsang,A., Storms,R. and Bulter,G.
TITLE Expressed sequence tags from Aspergillus niger cDNA library
JOURNAL Unpublished (2005)
COMMENT Contact: Tsang A
Centre for Structural and Functional Genomics
Concordia University
7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada
Tel: 514 848 2424 3405
Fax: 514 848 4504
Email: tsang@vax2.concordia.ca
POLYA=No. Location/Qualifiers
FEATURES
source
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/organism="Aspergillus niger"
/mol_type="mRNA"
/strain="N402"
/db_xref="taxon:5061"
/dev_stage="mycelial growth"
/lab_host="E. coli"
/clone="Asn_05863"
/clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
/note="Vector: pBluescript KS+; Site 1: XhoI; Site 2:
EcoRI; Complementary DNA was synthesized with ZAP Kit
(Stratagene) using poly(A)+RNA isolated from Aspergillus
niger cultured under different carbon sources (glucose,
maltose, xylose, lactose, sorbitol, xylan, and bran).
Synthesis was primed with oligo(dT)/XhoI primer. EcoRI
adaptors were ligated to the blunt-ended, double-stranded
cDNA. The EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp)."
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Db 420 ACCTCAACCACTTCATGCTTGGGCTAAGCTGGGAATGAACCTGGGTACTCACAACACTAC 479
QY 172 GlnileValAlaValGluGlyTyrPheSerSerglySerAlaSerileThrVal 189
Db 480 CAGATCGTGGCTACCGAGGGTTACCGAGACAGTGGATCTTCGTCCATCACTGTT 533

RESULT 13
DR702584 682 bp mRNA linear EST 14-JUL-2005
LOCUS Asn_02201 Aspergillus niger pBluescript (EcoRI-XhoI) Aspergillus
DEFINITION niger cDNA clone Asn_02201, mRNA sequence.
ACCESSION DR702584
VERSION DR702584
KEYWORDS DR702584.1 GI:70818875
SOURCE EST.
ORGANISM Aspergillus niger
Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 682)
AUTHORS Tsang,A., Storms,R. and Bulter,G.
TITLE Expressed sequence tags from Aspergillus niger cDNA library
JOURNAL Unpublished (2005)
COMMENT Contact: Tsang A
Centre for Structural and Functional Genomics
Concordia University
7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada
Tel: 514 848 2424 3405
Fax: 514 848 4504
Email: tsang@vax2.concordia.ca
POLYA=No. Location/Qualifiers
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1..682
/organism="Aspergillus niger"
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/clone="Asn_02201"
/dev_stage="mycelial growth"
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/note="Vector: pBluescript KS+; Site 1: XhoI; Site 2:
EcoRI; Complementary DNA was synthesized with ZAP Kit
(Stratagene) using poly(A)+RNA isolated from Aspergillus
niger cultured under different carbon sources (glucose,
maltose, xylose, lactose, sorbitol, xylan, and bran).
Synthesis was primed with oligo(dT)/XhoI primer. EcoRI
adaptors were ligated to the blunt-ended, double-stranded
cDNA. The EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp)."
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ORIGIN

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Alignment Scores:
Pred. No.: 5,496-60 Length: 682
Score: 623.50 Matches: 111
Percent Similarity: 77.09% Conservative: 27
Best Local Similarity: 62.01% Mismatches: 40
Query Match: 59.61% Indels: 1
Db: 8 Gaps: 1
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US-09-990-874b-55 (1-190) x DR702584 (1-682)

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QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
Db 149 ACCGGCGAGAACACCGGCTTCTACTACTCTCTGGACCGCGGGGTGGACGTGACC 208
QY 27 MetThrLeuGlyProGlyGlyValPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
Db 209 TACACCAACGAGATGCTGGTGTCTACATCTGTGAGTGGTCCACACGTGGCACTTTGTC 268
QY 47 GlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheserGlySerTyr 66
Db 269 GGTGGAAAGGGCTGGAAACCCCGGAAGTGGCAGGAC---ATCACCTACAGCGCACCTTC 325
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ORIGIN

```

Alignment Scores:
Pred. No.: 1,116-60 Length: 664
Score: 629.50 Matches: 113
Percent Similarity: 77.53% Conservative: 25
Best Local Similarity: 63.48% Mismatches: 39
Query Match: 60.18% Indels: 1
Db: 8 Gaps: 1
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US-09-990-874b-55 (1-190) x DR705641 (1-664)

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QY 12 GlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThrMetThrLeuGlyPro 31
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QY 32 GlyGlyGlnPheSerValAsnTrpSerAsnSerglyAsnPheValGlyGlyLysGlyTyr 51
Db 63 GCTGGTGCCTACACTGTTGAGTGTGTCACACGTGGGCACTTTGTCGTGGAAAGGCTGG 122
QY 52 GlnProGlyThrLysAsnLysValIleAsnPheserGlySerTyrAsnProAsnGlyAsn 71
Db 123 AACCCCGGAAGTGGCGCAGGAC---ATCACCTACAGCGGCACCTTCACCCCTAGCGGCAAC 179
QY 72 SerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeuIleGluTyrTyrIleValGlu 91
Db 180 GGCTACCTCTCCGTCTATGGCTGGACACTGACCTGACCTCTGATCGAGTACTACATCGTCGAG 239
QY 92 AsnPhesGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSerAsp 111
Db 240 TCCTACGGCGACTACACCCCGGAGTGGAGCGACGATACAGGCGACCGTCACTCGGAC 299
QY 112 GlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGluGlyThr 131
Db 300 GGATCCGTTTACGATATCTACACGGCTACCCCGTACCAATGCTGCTTCCATTCCAGGGAAC 359
QY 132 AlaThrPheTyrGlnTyrTrpSerValArgAsnArgArgSerSerGlySerValAsn 151
Db 360 GCTACTCTTCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
QY 152 ThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyr 171
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QY 67 AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeuLeuGlu 86
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QY 87 TyrTyrIleValGluAsnPhedGlyThrTyrAsnProSerThrGlyAlaThrIysHisGly 106
Db 386 TACTATACGTCTGAGTCTTACGCGCACTCAACCCCGGAGTGAGGCGACGTACAAGGCG 445
QY 107 GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
Db 446 ACCGTCACTCGAGCGATCCGGTTTACGATATCTACACGCTACCGTACCAATGCTGCT 505
QY 127 SerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgAsnArgSer 146
Db 506 TCAITTCAGGAACCGCTACCTTCACTCACTAGTACTGCTTGGCTTAAGTGGGAATGAACCTG 565
QY 147 SerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGlnGlyLeuThrLeu 166
Db 566 GCGGAACCGTTACCACTCCCAACCACTTCAATGCTTGGCTTAAGTGGGAATGAACCTG 625
QY 167 GlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAla 185
Db 626 GGTACTCAACAATACCAATACCGATCGTGGCTACGAGGGTTACAGAGCACTGATCTTCG 682

RESULT 14
A0160254/c
LOCUS
DEFINITION
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mgx00003L19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgx00003L19r, genomic survey sequence.
A0160254
A0160254.1 GI:3557243
GSS.
Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 750)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasiniowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 344.
Location/Qualifiers
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/mol_type="genomic DNA"
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/clone="mgx00003L19r"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

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ORIGIN
Alignment Scores:
Pred. No.: 7,12e-60 Length: 750
Score: 623.00 Matches: 120
Percent Similarity: 67.14% Conservative: 23
Best Local Similarity: 56.34% Mismatches: 39
Query Match: 59.56% Indels: 31
DB: 9 Gaps: 3
US-09-990-874B-55 (1-190) x A0160254 (1-750)
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QY 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSerAsnSerGlyAsnPheVal 46
Db 580 TACACATGAGCGGAGCGTGGTTCAGTTTTCGTACAGTGGCGGCACCGCGCACTTTGTTC 521
QY 47 GlyGlyLysGlyTyrGlnProGlyThr----- 55
Db 520 GGTGGAAAGGTTGGAAACCGGCAATGCTGGGTGAGTTTTTTGTTTGTCTTTTGTCTTA 461
QY 56 -----Lys-AsnLys 58
Db 460 TGTACTTTTCCCAAAAAAGGAAAAAAGAGACTAACCAACAACAACAAAAACAGCCG 401
QY 58 sValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrG 78
Db 400 CGTCATCAACTACTCGGGAGCTACAGCCCNAGGGCAACTCATCTACCTGGCCGCTACCG 341
QY 78 YTrpSerArgAsnProLeuIleGlyTyrTyrIleValGluAsnPheGlyThrTyrAsnPr 98
Db 340 CTGGAGCGGCAACCGCTGATCGTACTACGTGGTGGAGAGCTTTGGCAGCTACAACCC 281
QY 98 oSerThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCy 118
Db 280 GTCGTGGCGCGCCCAACCAACCGGGTCTTCACTCGGACGGCAGCACCTACGACATCCT 221
QY 118 sArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTr 138
Db 220 GGTACGACCCCGCTACACACCGCTTCATCCATCGGCGCACCAAGACCTTTCAGCAGTCTG 161
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QY 158 aTrpAlaArgGlnGlyLeuThrLeuGlyThrMet---AspTyrGlnIleValAlaValG 177
Db 100 CTGGCGCAACCGCGGCTCAACCTCGGCAACAGTGGAACTACCAATCTCTGGCCGCTCGA 41
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Db 40 GGGCTACCAACAGCGCGCTCCGCCAGCATGACTGTC 4
RESULT 15
CV496238
LOCUS
DEFINITION
73987.1 Cold Sweetening B Solanum tuberosum cDNA clone 73987 5',
mRNA sequence.
CV496238
CV496238.1 GI:53778595
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 712)
Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Laque, M., De
Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Frueki, G. and Regan, S.
Generation of ESTs from tubers following 3 months storage at 4

```

degrees celsius, and 95% relative humidity
Unpublished (2004)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..712
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/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="73987"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/clone_lib="Cold Sweetening B"
/note="Vector: pBluescript II SK(+). XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Developmental series. Plants from
pathogen-free Solanum tuberosum var. Shepody, clone 1756,
nuclear stock were grown in a screenhouse under natural
conditions. Mature, harvested tubers were stored in the
dark at 4C, 95% relative humidity for 3 months. RNA was
isolated for library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Alignment Scores:

Pred. No.:	7,566-60	Length:	712
Score:	622.50	Matches:	119
Percent Similarity:	79.03%	Conservative:	28
Best local Similarity:	63.98%	Mismatches:	35
Query Match:	59.51%	Indels:	4
DB:	7	Gaps:	3

US-09-990-874B-55 (1-190) x CV496238 (1-712)

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Db	181	GTCCGTGGAAAGGATGGGCTGTTGGTCCGAG---CGCTCCATCTCTTACACCGGATCC	237
Qy	66	TyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeuIle	85
Db	238	TACAAACCCACGGAACCTCTACCTCTCCGTCTATGGTTGGACTACCTCCCCCTCATC	297
Qy	86	GluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHis	105
Db	298	GAATACACTACTCGTCAAGACTTTGGACACTAGATCCCTCTCCGCCGCCACCGAATC	357
Qy	106	GlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAla	125
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Qy	126	ProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgAsnArgArg	145
Db	418	CCTTCGTTCAAGGAACCTGCTACCTTCAAGCAATACTGGTCCGTCCGTACTAGCAAGCGT	477
Qy	146	SerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGlnGlyLeuThr	165
Db	478	ACGAGCGGTACCGTCAACCTGCAAAACCATTTTCAGCCTGGAGAGTTGGATTGACT	537
Qy	166	LeuGly---ThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSer-SerGlySe	184
Db	538	TTGGGCTCAAGCTACAAAGTACCAATTTGCTTTGAGGGGTACCAAGCAAGTGTGTTTC	597

Qy	184	rAlaSerIleThrVal	189
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Search completed: December 30, 2005, 03:32:44
Job time : 3759 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2005, 01:16:22 ; Search time 165 Seconds
(without alignments)
2046.889 Million cell updates/sec

Title: US-09-990-874B-55
Perfect score: 1046
Sequence: 1 QTIQPGTGYHGDGYFSYWN.....YQIVAVEGYFSGSASITVS 190

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	90.6	573	2	US-08-709-912-18
2	948	90.6	573	2	US-09-047-370-18
3	946	90.4	1015	2	US-08-121-436A-1
4	919	87.9	822	3	US-09-254-733-8
5	687	65.7	1281	3	US-08-768-373-1
6	687	65.7	1281	3	US-09-849-242A-1
7	643.5	61.5	983	2	US-08-886-765-1
8	643.5	61.5	983	3	US-09-115-660-1
9	635	60.7	1174	3	US-08-768-373-3

10	635	60.7	1174	3	US-09-849-242A-3	Sequence 3, Appli
11	629.5	60.2	1219	2	US-08-230-979A-7	Sequence 7, Appli
12	611.5	58.5	1375	3	US-08-468-812-1	Sequence 1, Appli
13	611.5	58.5	1375	3	US-08-590-563-1	Sequence 1, Appli
14	611.5	58.5	1375	3	US-09-770-621-1	Sequence 1, Appli
15	611.5	58.5	1375	3	US-09-235-832-1	Sequence 1, Appli
16	609	58.2	927	2	US-08-507-431-5	Sequence 5, Appli
17	609	58.2	927	2	US-08-902-655A-5	Sequence 5, Appli
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19	609	58.2	927	3	US-09-219-277-5	Sequence 5, Appli
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21	605.5	57.9	2898	3	US-09-462-246-1	Sequence 1, Appli
22	602.5	57.6	1123	2	US-08-458-023B-3	Sequence 3, Appli
23	601.5	57.3	2055	3	US-08-367-891A-1	Sequence 1, Appli
24	557	53.3	675	2	US-07-744-570B-1	Sequence 1, Appli
25	537.5	51.4	847	3	US-09-260-283-1	Sequence 1, Appli
26	537.5	51.4	1244	3	US-08-591-685-12	Sequence 12, Appli
27	525.5	50.2	1207	2	US-08-575-964-2	Sequence 2, Appli
28	525.5	50.2	1207	2	US-08-963-500-2	Sequence 2, Appli
29	521	49.8	744	3	US-09-189-060B-11	Sequence 11, Appli
30	501.5	47.9	642	2	US-08-104-445-2	Sequence 2, Appli
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35	496	47.4	579	2	US-08-709-912-19	Sequence 19, Appli
36	496	47.4	579	2	US-09-047-370-19	Sequence 19, Appli
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41	489	46.7	744	3	US-08-470-953A-4	Sequence 4, Appli
42	489	46.7	744	3	US-08-470-953A-5	Sequence 5, Appli
43	489	46.7	871	2	US-08-698-978-1	Sequence 1, Appli
44	489	46.7	1513	3	US-08-470-953A-10	Sequence 10, Appli
45	489	46.7	1513	3	US-08-470-953A-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-08-709-912-18
; Sequence 18, Application US/08709912
; Patent No. 5759840
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,912
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr. Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pTVX(3-190)
US-08-709-912-18

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Pred. No.: 2,448-98 Length: 573
Score: 948.00 Matches: 174
Percent Similarity: 95.24% Conservative: 6
Best Local Similarity: 92.06% Mismatches: 9
Query Match: 90.63% Indels: 0
DB: 2 Gaps: 0

US-09-990-874B-55 (1-190) x US-08-709-912-18 (1-573)

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QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsn 41
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RESULT 2

US-09-047-370-18
Sequence 18, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto

APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pTVX(3-190)
US-09-047-370-18

Alignment Scores:
Pred. No.: 2,448-98 Length: 573
Score: 948.00 Matches: 174
Percent Similarity: 95.24% Conservative: 6
Best Local Similarity: 92.06% Mismatches: 9
Query Match: 90.63% Indels: 0
DB: 2 Gaps: 0

US-09-990-874B-55 (1-190) x US-09-047-370-18 (1-573)

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DB 3 AGCATAGGACCCAGGAAACCGGTTTCAACAACCGGTACTTTTACAGCTATTGGACGATGCG 62
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsn 41
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QY 42 SerGlyAsnPheValGlyGlyTyrGlnProGlyThrLysAsnLysValIleAsn 61
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QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGly 101
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APPLICANT: AOYAGI, KAORU
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 822
TYPE: DNA
ORGANISM: TRICHODERMA VIRIDE MC300-1
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LOCATION: (413)..(809)
US-09-254-733-8

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Best Local Similarity: 75.54% Mismatches: 9
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DB: 3 Gaps: 1

US-09-990-874B-55 (1-190) x US-09-254-733-8 (1-822)

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DB 593 CGCAGCGAGCGCGCTCAACCGCGCGTCCATCGAGGGCACCTCCACCTTTTACCACTACTG 652
QY 138 pSerValArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAl 158
DB 653 GTCCGTCCGCGCGCACCCACCGCTCCAGCGGCTCCGTCAACGCGGACCACTTCCACGC 712
QY 158 atrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluG1 178
DB 713 GTGGGCTTCGACGCGCTGACGCTGGGCAACCATGATTAACAGATTGTTCGCGTGAGGG 772
QY 178 YTrpPheSerSerGlySerAlaSerIleThrValSer 190
DB 773 CTACTTTAGCTCTGGCTCTGCTTCATCACCCTCAGC 809

RESULT 5

US-08-768-373-1
Sequence 1, Application US/08768373
Patent No. 6228629
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: M NTYL, ARJA
APPLICANT: VEHMAANPER, JARI
APPLICANT: LANTTO, RAUJA
APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIRKKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNES, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:

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/ ORGANISM: Chaetomium thermophilum
/ STRAIN: CBS730.95
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 195..423
/ OTHER INFORMATION: /product= "XLNA"
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 483..1039
/ OTHER INFORMATION: /product= "XLNA"
US-08-768-373-1

Alignment Scores:
Pred. No.: 3,1e-68 Length: 1281
Score: 687.00 Matches: 126
Percent Similarity: 72.86% Conservative: 27
Best Local Similarity: 60.00% Mismatches: 36
Query Match: 65.68% Indels: 22
DB: 3 Gaps: 2

US-09-990-874B-55 (1-190) x US-08-768-373-1 (1-1281)

QY 1 GlnThrIle---GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsn 19
Db 273 CAGACGCTCACCAGCAGTGCACCGGCACCCACCAATGGCTACTACTACAGCTTCTGGACC 332

QY 20 AspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValaenTtp 39
Db 333 GATGGCCAAAGGCAACATTCGTTCAACCTCGAGAGCGGTGGCAGTACAGCGTGACATGG 392

QY 40 SerAsnSerGlyAsnPheValGlyGlyLys----- 49
Db 393 TCTGGTAACGGCACTGGGTGTCGGGCAA-AGGTATGTCCTCTTAATGTTTCCAGCGCTA 451

QY 50 -----GlyTtpGlnProGlyThrLysAsnLysVal 59
Db 452 TCGAATGAACCTAAATGCTAACTGTTTAAACAGGCTGGAAACCCCGGTACCGATACCGTGT 511

QY 60 IleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTtp 79
Db 512 ATCACTACACAGCCGCACTACAGACCAACGGCACTCTCTTACTCGCGCTACGGCTGG 571

QY 80 SerArgAsnProLeuIleGlyTyrTyrIleValGluAsnPheGlyThrTyrAsnProSer 99
Db 572 ACCCGCAACCCGCTGATCGAGTACTAGTGTCTGAGAGCTTCGGCACTTACGACCGCTG 631

QY 100 ThrGlyAlaThrIleHisGlyGluValThrSerAspGlySerValTyrAspIleCysArg 119
Db 632 ACGGGCGCCACCGCATGGCGGCTGACCCAGCGGCGGACCTTACCAACATCTACCGC 691

QY 120 ThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTtpSer 139
Db 692 ACGCAGCGGTCAACCGCCCTCCATCGAGGCGGCAACCAAGACCTTCTACCAATCTGCT 751

QY 140 ValArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTtp 159
Db 752 GTGCGCACCTCCAGCGCAGCGCGGTACTGTTCATGCGCAACCACTTCATGTGG 811

QY 160 AlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db 812 AGCGAGGCTGCTCGCAGCTGGGTTCCTCATGATTATCAGATTGTGGCTACTGAGGGTTAC 871

QY 180 PheSerSerGlySerAlaSerIleThrVal 189
Db 872 TACTCGTCTGGCTCGGCGCACTGTCATGTT 901

RESULT 6
US-09-849-242A-1
; Sequence 1, Application US/09849242A
; Patent No. 6635464
; GENERAL INFORMATION:
; APPLICANT: PALOHEIMO, MARJA
; HAKOLA, SATU

MONTILO, ARJA
VEHMAANPERO, JARI
LANTTO, RAIJA
LAHTINEN, TARJA
FAGERSTRM, RICHARD
SUONINEN, PIIRKO

TITLE OF INVENTION: NOVEL XILANASES, GENES ENCODING THEM,
AND USES THEREOF

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION: /product= "XLNA"
FEATURE:
NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /product= "XLNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-849-242A-1

Alignment Scores:
Pred. No.: 3,1e-68 Length: 1281
Score: 687.00 Matches: 126
Percent Similarity: 72.86% Conservative: 27
Best Local Similarity: 60.00% Mismatches: 36
Query Match: 65.68% Indels: 22
DB: 3 Gaps: 2

US-09-990-874B-55 (1-190) x US-09-849-242A-1 (1-1281)

QY 1 GlnThrIle---GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsn 19
Db 273 CAGACGCTCACCAGCAGTGCACCGGCACCCACCAATGGCTACTACTACAGCTTCTGGACC 332
```

QY 20 AspGlyHisGlyClyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyr 39
Db 333 GATGGCCAAAGGCAACATTCGTTCAACCTCGAGAGCGGTGGCCGTACAGCGTGACATGG 392
QY 40 SerAsnSerGlyAsnPheValGlyGlyLys----- 49
Db 393 TCTGGTAAACGGCAACTGGGTGGCGCAA-AGGTATGTCTCTTAATGTTTCCAGCGCTA 451
QY 50 -----GlyTyrGlnProGlyThrLysAsnLysVal 59
Db 452 TGGATGAACCTAAATGCTAACTGTTAAACAGCGGTGAACCCCGGTACCGATACCGGTGC 511
QY 60 IleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyr 79
Db 512 ATCAACTACACAGCCCACTACAGACCAACGGCACTCTTACTCTCCGCTCTACGGCTGG 571
QY 80 SerArgAsnProLeuIleGlyTyrIleValGluAsnPheGlyThrTyrAsnProSer 99
Db 572 ACCCGCAACCCGCTGATCGAGTACTAGTGTGCGAGAGCTTCGGCACTTACGACCCGTCG 631
QY 100 ThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspLysCysArg 119
Db 632 ACGGGCGCACCGCATGGCGAGCGTGACCCAGCGCGGCACCTTACCAACATCTACCGC 691
QY 120 ThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSer 139
Db 692 ACGAGCGGTCAACCGCCCTCCATCGAGGCGCAACAGACCTTACCACTACTGCTT 751
QY 140 ValArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyr 159
Db 752 GTGGGACCTCCAGCGCACCGCGGTACTGTTACCATGGCCCAACCACTTCAATGCTTG 811
QY 160 AlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db 812 AGCAGCGCTGCTGCGAGCTGGGTCCCATGATTATCAGATTGTGCTACTGAGGGTTAC 871
QY 180 PheSerSerGlySerAlaSerIleThrVal 189
Db 872 TACTGCTGCGCTCGCGGACTGTCAATGTT 901

RESULT 7

US-08-886-765-1
; Sequence 1, Application US/08886765
; Patent No. 5817500
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; APPLICANT: Wagner, Peter
; APPLICANT: Mullertz, Anette
; APPLICANT: Knap, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5817500 No. 5817500disk of No. 5817500th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Thermomyces lanuginosus
; STRAIN: DSM 4109
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..705
; US-08-886-765-1

Alignment Scores:
Pred. No.: 1,828-63 Length: 983
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 2 Gaps: 1

US-09-990-874B-55 (1-190) x US-08-886-765-1 (1-983)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
Db 124 CAGACAACCCCACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGAC 193
QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40
Db 184 GTGGAGCGCGCCAGCTACCAACCTGGGAAGCGGCACCTACGAGATCAGCTGGGA 243
QY 41 AsnSerGlyAsnPheValGlyGlyTyrGlnPheGlyThrLysAsnLysValIle 60
Db 244 GATGCGGTAACTCGTGGTGGAAAGGCTGGAACCCCGCGCTGAACCAAGAGCCATC 303
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSer 80
Db 304 CACTTTGAGGGTGTTCACGACCAACGGCAACAGCTACTTCGGGTCTACGGTTGGACC 363
QY 81 ArgAsnProLeuIleGlyTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
Db 364 CGCAACCCGCTGCTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTCTCTCC 423
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspLysCysArgThr 120
Db 424 GGTGCTACCGATCTAGGAACCTGTCGAGTCGACGCGTAGCATCTATCGACTCGCAAGACC 483
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerVal 140
Db 484 ACTCGCGTCAACGCACTAGCATCGACGCGCACCCAAACCTTCGACCAATCTGTCGTC 543
QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAla 160
Db 544 CGCCAGGACAGCGGCACACCGGTACCGTCCAGACGGGCTGGCCACTTCGACGCGCTGGCT 603
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db 604 CGCGCTGCTTGAATGTCAACGCTGACCACTACTACCATCGTTCGATCGTTCGACGGGCTAC 663
QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
Db 664 TTCAGCAGCGGCTATGCTCGCATCACCCTGCTTGTCT 696

RESULT 8

US-09-115-660-1
; Sequence 1, Application US/09115660
; Patent No. 6245546
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp

APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No. 62455460 No. 62455460disk of No. 6245546th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,660
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/886,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambirie, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324-204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Thermomyces lanuginosus
STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705
US-09-115-660-1
Alignment Scores:
Pred. No.: 1.82e-63 Length: 983
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 3 Gaps: 1
US-09-990-874b-55 (1-190) x US-09-115-660-1 (1-983)
QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 124 CAGACAAACCCCACTCGGAGGGCTGGCAGCATGGTTATTATCTCTGGTGGAGTGAC 183
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 184 GGTGAGCGCAGGCACAGTACACCAACCTGGAGGGGACCTACGAGATCAGCTGGGA 243
QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlyGlnPheGlnProGlyThrLysAsnLysValle 60
DB 244 GATGCGGTAACTCGTGGTAAAGGCTGGAAACCCCGGCTGAAACCAAGAGGACATC 303
QY 61 AsnPheSerGlySerTyrAsnProGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 304 CACTTTGAGGGTGTATTACAGCCAAACGCGACAGCTACCTTCGCGGTCTACCGTTGGACC 363
QY 81 ArgAsnProIleGlyTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100

DB 364 CGCAACCGCTGGTGGAGTATTATCATCTCGAGAACTTGGCACTATGATCTTCTCTCC 423
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 424 GGTGCTACCGATCTAGGAACGTGCGAGTGGCAGCGTAGCATCTATCGACTCGGCAAGACC 483
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 484 ACTCGCGTCAACGACCTAGCATCGACGGCAACCCCAACCTTCGACCAATATCTGGTGGTGC 543
QY 141 ArgArgAsnArgAspSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 544 CGCAGGCAAGCGCACCGAGGTACCTCGACGGGCTGCCACTTCGACGCTGGGCT 603
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 604 CGCGCTGGTTGAATGTCAACGGTGACCACTACTACCAAGATCGTTGCAACGAGGGCTAC 663
QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
DB 664 TTCAGCAGCGCTATGCTCGCATCACCGTTGCT 696
RESULT 9
US-08-768-373-3
; Sequence 3, Application US/08768373
; Patent No. 6228629
; GENERAL INFORMATION:
; APPLICANT: PALOHEIMO, MARJA
; APPLICANT: HAKOLA, SATU
; APPLICANT: M NTYL, ARJA
; APPLICANT: VEHMAANPER, JARI
; APPLICANT: LANTTO, RAIJA
; APPLICANT: LAHTINEN, TARJA
; APPLICANT: PAGERSTR, M, RICHARD
; APPLICANT: SUOMINEN, RIKKO
; TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/768,373
; FILING DATE: 17-DEC-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,746
; FILING DATE: 18-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,839
; FILING DATE: 28-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CIMBALA, MICHELE A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0540003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CB8730.95
FEATURE:
NAME/KEY: exon
LOCATION: 204..472
OTHER INFORMATION: /product= "XLNB"
FEATURE:
NAME/KEY: exon
LOCATION: 537..960
OTHER INFORMATION: /product= "XLNB"
US-08-768-373-3

Alignment Scores:
Pred. No.: 2,16e-62 Length: 1174
Score: 635.00 Matches: 120
Percent Similarity: 69.76% Conservative: 23
Best Local Similarity: 58.54% Mismatches: 41
Query Match: 60.71% Indels: 21
DB: 3 Gaps: 2

US-09-990-874B-55 (1-190) x US-08-768-373-3 (1-1174)

QY 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAspGlyHisGlyGlyVal 25
DB 336 GGCACGGGCACACACACGGGTGGTATTACTCTCTCGACCGCGCGCGCGCGGTG 395
QY 26 ThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSerAsnSerGlyAsnPhe 45
DB 396 TGGTACACCAATGTAATGGCGGTTCGTATAGTGTGAACCTGGCAGAACTGTGGAAATTTT 455
QY 46 ValGlyGlyValGlyTyrPheTyrSerValAsnTyrSerAsnTyrSerAsnTyrSer 57
DB 456 GTCCGCGGAAAGGATGGTAAAGCTACTGTCCACCGGACACTGAAACTTATAGTCCGCGC 515
QY 58 -----LysValIleAsnPheSerGlySe 65
DB 516 CAGATGCTGACCTCTCTCCAGCGCGCACCGCGCGCAACGATCAATACTCTCGGCAA 575
QY 65 rTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeu1 85
DB 576 CTACAACCGTCCGGCAACAGCTACTCTCGCATCTACGGCTGGACGCGCAACCCCTGCT 635
QY 85 eGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrIlyshi 105
DB 636 TGAGTACTACATCGTTCGAGTCTGACGCACTTACGATCCGTCGCGCGCGCCAGAACTT 695
QY 105 sGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAl 125
DB 696 GGGCATTCTCCAGTCGAGCGGGGACGTACAGATCGCCAGAGCAGCGCGGTACATGC 755
QY 125 aProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgAsnArgAr 145
DB 756 TCCTCAATCGAAGGAACCAAGACGTTTACGAGTATTGAGCGCTGAGGACGCTCAAGCG 815
QY 145 gSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGlnGlyLeuTh 165
DB 816 GGTGGAGGACCGGTACCGGTTTCGCAACCACTTCAATGCTTGAAGAGTAAGGGGTGAA 875
QY 165 rLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAl 185
DB 876 TTGGGTAGCCACGATTATCAGATTGTGGCGACTGAGGGTTATAGAGTAGTGGGTCCGC 935
QY 185 aSerIleThrVal 189
DB 936 TTCGATTACTGTT 948

RESULT 10

US-09-849-242A-3
; Sequence 3, Application US/09849242A
; Patent No. 6635464

GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
HAKOLA, SATU
MONTYLO, ARJA
VEHMAANPERO, JARI
LANTTO, RAIJA
LAHTINEN, TARJA
FAGERSTRM, RICHARD
SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,951
REFERENCE/POCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1174 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CB8730.95
FEATURE:
NAME/KEY: exon
LOCATION: 204..472
OTHER INFORMATION: /product= "XLNB"
FEATURE:
NAME/KEY: exon
LOCATION: 537..960
OTHER INFORMATION: /product= "XLNB"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-849-242A-3

Alignment Scores:
Pred. No.: 2,16e-62 Length: 1174
Score: 635.00 Matches: 120
Percent Similarity: 69.76% Conservative: 23
Best Local Similarity: 58.54% Mismatches: 41
Query Match: 60.71% Indels: 21
DB: 3 Gaps: 2

US-09-990-874B-55 (1-190) x US-09-849-242A-3 (1-1174)

QY 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTTPAsnAspGlyHisGlyGlyVal 25
Db 336 GGCACGGGCACACACACGGGTGGTATTACTCTCTGGACCGACGGCGGGCGACGGTG 395
QY 26 ThrMetThrLeuGlyProGlyGlnPheSerValAsnTTPSerAsnSerGlyValPhe 45
Db 396 TGGTACCAATGGTAATGGCGGTGGTATAGTGGAACTGGCAGAACCTGTGGAAATTTT 455
QY 46 ValGlyGlyValGlyTTP-----GlnProGly-ThrLysAsn----- 57
Db 456 GTCCGCGGAAGGATGGTAAGCTCACTCTCCACCGGACACTGAAACTTAGTGGCGAGC 515
QY 58 -----LysValIleAsnPheSerGlySe 65
Db 516 CAGATGCTGACCTCTGTCCAGCGCACCGCGCGACCGCAACAGATCAAAATACTCTCGGCAA 575
QY 65 rTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTTPSerArgAsnProLeu1 85
Db 576 CTACAAACCGTCCGGCNAACAGGTACTCTGCCATCTACGGCTGGACCGCAACCCCTGGT 635
QY 85 eGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHi 105
Db 636 TGAGTACTACATCGTCAGTCTGACGGCACTTACGATCGCTGCGGGCGCCAGACTT 695
QY 105 sGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAl 125
Db 696 GGGACATTCAGTCCGACGGCGGGACGTACAAGATCGCAAGAGCACCGGTACAAATGC 755
QY 125 aProSerIleGluGlyThrAlaThrPheTyrGlnTyrTTPSerValArgAsnArgAr 145
Db 756 TCCCTCAATCGAAGGAACCAACAGCGTTTACGAGTATTGGAGCGTGAGACGTCAAAGCG 815
QY 145 gSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTTPAlaArgGlnGlyLeuTh 165
Db 816 GGTGAGGACACGGTGACCGTTCGGAACCATTTCAATGCTTGGACAGTAAGGGTTGAA 875
QY 165 rLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAl 185
Db 876 TTTGGGTAGCCACGATTATCAGATTGTGGCGACTGAGGGTTTAAAGTAGTGGGTGGC 935
QY 185 aSerIleThrVal 189
Db 936 TTCGATTACTGT 948

RESULT 11

US-08-290-979A-7
; Sequence 7, Application US/08290979A
; Patent No. 5610046
; GENERAL INFORMATION:
; APPLICANT: VAN OIJEN, Albert J.H.
; APPLICANT: DE GRAAFF, Leendert H.
; APPLICANT: VAN DEN BROECK, Henriette C.
; APPLICANT: VISSER, Jacob
; TITLE OF INVENTION: Cloning and Expression of Xylanase B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,979A
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KATE H. MURASHIGE

REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0045.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MSN FOERS WSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Aspergillus tubigenensis
STRAIN: DS16813
FEATURE:
NAME/KEY: CDS
LOCATION: join(902..1180, 1248..1643)
US-08-290-979A-7

Alignment Scores:

Pred. No.:	2,268-61	Length:	2219
Score:	629.50	Matches:	116
Percent Similarity:	71.22%	Conservative:	30
Best Local Similarity:	56.59%	Mismatches:	37
Query Match:	60.18%	Indels:	22
DB:	2	Gaps:	1

US-09-990-874B-55 (1-190) x US-08-290-979A-7 (1-2219)

QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTTPAsnAspGlyHisGlyGlyValThr 26
Db 1028 ACCGCGGAGAACACCGGCTTCTACTACTCTCTGGACCGACGGCGGTGTGTGACC 1087
QY 27 MetThrLeuGlyProGlyGlnPheSerValAsnTTPSerAsnSerGlyValAsnPheVal 46
Db 1088 TACACCAACGGGTGACGGCTGCGTACACCGTGGAGTGGTGTGTGCAACGTTGGCACTTTGTT 1147
QY 47 GlyGlyLysGlyTTPGlnProGlyThr-LysAsnLysVal----- 59
Db 1148 GGTGGAAAGGCTGGAAACCTCGAAGTGGCAGTAAGTTAACCTTTCCCAAGCTGTCCT 1207
QY 60 -----IleAsnPheSerGlySe 65
Db 1208 CTAGGGTATTCACTGAAACAAATGCTCACATAACTTCAGGGACATCACCTACAGCGGCAC 1267
QY 65 rTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTTPSerArgAsnProLeu1 85
Db 1268 CTTTACCCCTAGCGCAACGGCTACTCTCGGTCTATGGCTGGACCACTGACCCCTGAT 1327
QY 85 eGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHi 105
Db 1328 CGAGTACTACATCGTGGAGTCTTACGGCACTACAAACCCCGGACGTGGAGGACCTTACAA 1387
QY 105 sGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAl 125
Db 1388 GGGCAGCGTCACTCCGATGGATCCGCTTACGATATCTACAGGCTTACCGGCTACCGCAACGC 1447
QY 125 aProSerIleGluGlyThrAlaThrPheTyrGlnTyrTTPSerValArgAsnArgAr 145
Db 1448 CGCTTCCATCCAAAGGAACCGCTTACCTTACCAGTACTCGTTCGCTGGCAGAACAGAG 1507
QY 145 gSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTTPAlaArgGlnGlyLeuTh 165
Db 1508 ATCGGAGGAACTGTATCCACTTCCACCACTTCCACCGTTTGGGCTAAGCTGGGCATGAA 1567
QY 165 rLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAl 185
Db 1568 CTGGGTACTCACAACTACCAATCGTGGCTACCGAGGGCTACCGAGGACGCGGATCTTC 1627
QY 185 aSerIleThrVal 189

Db 1628 CTCATCACTGTT 1640

RESULT 12

US-08-468-812-1

; Sequence 1, Application US/08468812

; Patent No. 5935836

; GENERAL INFORMATION:

; APPLICANT: Vehmaanper, Jari

; APPLICANT: M ntyl, Arja

; APPLICANT: Fagerstr m, Richard

; APPLICANT: Lantto, Raija

; APPLICANT: Paloheimo, Marja

; APPLICANT: Suominen, Pirkko

; APPLICANT: Lahtinen, Tarja

; APPLICANT: Kristo, Paula

; TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods

; TITLE OF INVENTION: of Use

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLSTEIN & FOX

; STREET: 1100 New York Ave., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,812

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/332,412

; FILING DATE: 31-OCT-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/282,001

; FILING DATE: 29-JUL-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Bugalsky, Larry B.

; REGISTRATION NUMBER: 35,086

; REFERENCE/DOCKET NUMBER: 1050.0340002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1375 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 303..1334

US-08-468-812-1

Alignment Scores:

Pred. No.: 1.25e-59

Score: 611.50

Percent Similarity: 75.94%

Best Local Similarity: 57.75%

Query Match: 58.46%

DB: 2

US-09-990-874B-55 (1-190) x US-08-468-812-1 (1-1375)

Qy 4 GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGly 23

Db 447 CAGAACACGCGGTACGACACCGCTACTCTTCTGACCGACCGCGCGCGG 506

Qy 24 GlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGly 43

Db 507 ACCGTCCTCATGACCTCTCACTCGGCGCGAGCTACAGCACCTCTGCGGGACACCGGG 566

Qy 44 AsnPheValGlyGlyLysGlyTyrPheGlnProGlyThrLysAsnLysValleAsnPheSer 63

Db 567 AACTTCGTGCGCGGCAAGGGCTGGTCCACCGGGGACGG---CGGACCGCTGACCTACAC 623

Qy 64 GlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnPro 83

Db 624 GCCTCTTCAACCCCTCGGCTAAGCGCTACCTCTACGGCTTACGGCTGGACCGAGAACCG 683

Qy 84 LeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103

Db 684 CTCGTGAGTACTACATCGTCGAGAGCTGGGCGACCTACCGGCGCC---ACCGGCACCTAC 740

Qy 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123

Db 741 AAG---GGCACCGTCAACCCAGCGGGAACGTACGACATCTACGAGACCTGGCGCGTAC 797

Qy 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgArgAsn 143

Db 798 AACGCGCGCTCCATCGAGGCGCACCGGACCTTCCAGCAGTCTTGGAGCGTTCGGCAGCAG 857

Qy 144 ArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGly 163

Db 858 AAGCGGACCGAGCGGACCATCATCCATCGGCAACCATCTCGACGCTTGGCGCGCGCGGC 917

Qy 164 LeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGly 183

Db 918 ATGAACCTGGGCGAGCACGACTACCATGATCATGGGCGACCGAGGCTTACGAGACGCGGT 977

Qy 184 SerAlaSerIleThrValSer 190

Db 978 AGCTCCACCGCTCCATCAGC 998

RESULT 13

US-08-590-563-1

; Sequence 1, Application US/08590563

; Patent No. 6300114

; GENERAL INFORMATION:

; APPLICANT: M ntyl, Arja

; APPLICANT: Vehmaanper, Jari

; APPLICANT: Fagerstr m, Richard

; APPLICANT: Lantto, Raija

; APPLICANT: Paloheimo, Marja

; APPLICANT: Suominen, Pirkko

; APPLICANT: Lahtinen, Tarja

; TITLE OF INVENTION: Production and Secretion of Proteins of

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSSTEIN & FOX, P.L.L.C.

; STREET: 1100 New York Ave., N.W. Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/590,563

; FILING DATE: 26-JAN-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/468,812

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 536

Tue Jan 3 10:53:42 2006

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/332,412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282,001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 1050.0340003
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1375 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 303..1334
/
US-08-590-563-1
Alignment Scores:
Pred. No.: 1,25e-59 Length: 1375
Score: 611.50 Matches: 108
Percent Similarity: 75.94% Conservative: 34
Best Local Similarity: 57.75% Mismatches: 42
Query Match: 58.46% Indels: 3
DB: 3

US-09-990-874B-55 (1-190) x US-08-590-563-1 (1-1375)
Qy 4 GlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGly 23
Db 447 CAGAACCGGCGGTACGACGCGTACTTCTGACCGCGCGCGCGG 506

Qy 24 GlyValThrMetLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGly 43
Db 507 ACCGTCCTCATGACCTCCACTCGGCGCGCGTACGACGCGTCTGCGGCGGACACCGG 566

Qy 44 AsnPheValGlyGlySerGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSer 63
Db 567 AACTTCGTCCGCGCAAGCGGTGGTCCACCGGCGGACCGG---CGGACCGGTGACCTACAC 623

Qy 64 GlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnPro 83
Db 624 GCCTCTTCAACCGCGGTACGCGTACCGTACCTACCGTCTACGCGTGGACCGACCGCG 683

Qy 84 LeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103
Db 684 CTCGTCGAGTACTACATCGTCGAGAGCTGGGCGCACCTACCGGCC---ACCGCGACCTAC 740

Qy 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123
Db 741 AAG---GGCACCCTCACCAACCGCGGGAACGTACGACATCTACGAGACCTGGCGGTAC 797

Qy 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsn 143
Db 798 AACGCGCGCTCCATCAGGCGGACCGCGGACCTTCCAGCAGTCTTGGAGCGTCCGCGACGAG 857

Qy 144 ArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGly 163
Db 858 AAGCGGACCGGCGGACCATCATCGCAACCACTTCGACGCTGGCGCGCGCGCGCGC 917

Qy 164 LeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGly 183
Db 918 ATGAACCTGGCGGACCGCACGACGATACGATCATGCGCGGCGGCGGTCTACGAGCAGCGGT 977

Qy 184 SerAlaSerIleThrValSer 190
Db 978 AGTCCACCGTCTCCATCAGC 998

RESULT 14
US-09-770-621-1
/ Sequence 1, Application US/09770621
/ Patent No. 6506593
/ GENERAL INFORMATION:
/ APPLICANT: M ntyl , Arja
/ APPLICANT: Vehmaanper , Jari
/ APPLICANT: Pagarstr m, Richard
/ APPLICANT: Lantto, Raija
/ APPLICANT: Paloheimo, Marja
/ APPLICANT: Suominen, Pirkko
/ APPLICANT: Lahtinen, Tarja
/ TITLE OF INVENTION: Production and Secretion of Proteins of
/ NUMBER OF SEQUENCES: 39
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
/ STREET: 1100 New York Ave., N.W. Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/770,621
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/590,563
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/332,412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282,001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 1050.0340003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1375 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: No. 6506593 Relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 303..1334
/
US-09-770-621-1
Alignment Scores:
Pred. No.: 1,25e-59 Length: 1375
Score: 611.50 Matches: 108
Percent Similarity: 75.94% Conservative: 34
Best Local Similarity: 57.75% Mismatches: 42
Query Match: 58.46% Indels: 3
DB: 3
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US-09-990-874B-55 (1-190) x US-09-770-621-1 (1-1375)
QY 4 GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAspGlyHisGly 23
Db 447 CAGAACCAAGCGGGTACGACAAACGGCTACTTCTGTTCTGGACCGCGCCCGGG 506
QY 24 GlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGly 43
Db 507 ACCGTCCTCATGACCTCCACTCGGGCGGCACTACAGCACCTCTGGCGGAACACCGGG 566
QY 44 AsnPheValGlyGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSer 63
Db 567 AACTTCGTTCGCGGCAAGGGCTGGTCCACCGGGGACCG---CGGACCGCTGACCTACCAAC 623
QY 64 GlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnPro 83
Db 624 GCCTCCTTCAACCGGTCGGGGTAACGGCTACCTTCACGCTCTACGGCTGGACCGAGAACCGG 683
QY 84 LeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103
Db 684 CTCGTCGAGTACTACATCGTCGAGAGCTGGGCGACCTACCGGCC---ACCGGCACCTAC 740
QY 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123
Db 741 AAG---GGCACCGTCCACCGGCAAGGGTGGTCCACCGGGGACCG---CGGACCGCTGACCTACCAAC 797
QY 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgAsn 143
Db 798 AACGCGCGCTCATCGAGGGCAACCGGACCTTCCAGAGCTTCGAGCGCTCGGCGAGCGAG 857
QY 144 ArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGly 163
Db 858 AAGCGGACACCGGCAACCATCATCGGCAACCTTCGAGCGCTGGCGCCCGCGCGCG 917
QY 164 LeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGly 183
Db 918 ATGAACCTGGGCGACCGACTTACCAGATCATCGGCGGACCGAGGGCTACCGAGCGAGCGGT 977
QY 184 SerAlaSerIleThrValSer 190
Db 978 AGCTCCACCGTCTCCATCAGC 998

RESULT 15
US-09-235-832-1
; Sequence 1, Application US/09235832
; Patent No. 6667170
; GENERAL INFORMATION:
; APPLICANT: M ntyl , Arja
; APPLICANT: Vehmaanper , Jari
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lahtinen, Tarja
; TITLE OF INVENTION: Production and Secretion of Proteins of
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,832
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. 6667170 Relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-09-235-832-1

Alignment Scores:
Pred. No.: 1,25e-59 Length: 1375
Score: 611.50 Matches: 108
Percent Similarity: 75.94% Conservative: 34
Best Local Similarity: 57.75% Mismatches: 42
Query Match: 58.46% Indels: 3
DB: 3 Gaps: 3

US-09-990-874B-55 (1-190) x US-09-235-832-1 (1-1375)
QY 4 GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAspGlyHisGly 23
Db 447 CAGAACCAAGCGGGTACGACAAACGGCTACTTCTGTTCTGGACCGCGCCCGGG 506
QY 24 GlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGly 43
Db 507 ACCGTCCTCATGACCTCCACTCGGGCGGCACTACAGCACCTCTGGCGGAACACCGGG 566
QY 44 AsnPheValGlyGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSer 63
Db 567 AACTTCGTTCGCGGCAAGGGCTGGTCCACCGGGGACCG---CGGACCGCTGACCTACCAAC 623
QY 64 GlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnPro 83
Db 624 GCCTCCTTCAACCGGTCGGGGTAACGGCTACCTTCACGCTCTACGGCTGGACCGAGAACCGG 683
QY 84 LeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103
Db 684 CTCGTCGAGTACTACATCGTCGAGAGCTGGGCGACCTACCGGCC---ACCGGCACCTAC 740
QY 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123
Db 741 AAG---GGCACCGTCCACCGGCAAGGGTGGTCCACCGGGGACCG---CGGACCGCTGACCTACCAAC 797
QY 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgAsn 143
Db 798 AACGCGCGCTCATCGAGGGCAACCGGACCTTCCAGAGCTTCGAGCGCTCGGCGAGCGAG 857
QY 144 ArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGly 163
Db 858 AAGCGGACACCGGCAACCATCATCGGCAACCTTCGAGCGCTGGCGCCCGCGCGCG 917
QY 164 LeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGly 183
Db 918 ATGAACCTGGGCGACCGACTTACCAGATCATCGGCGGACCGAGGGCTACCGAGCGAGCGGT 977
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Db 918 ATGAACCTGGGCAGCCACGACTACGAGATCATGGCGACCGAGGGCTACCGAGCAGCGGT 977

Qy 184 SerAlaSerIleThrValSer 190

Db 978 AGCTCCACCGTCTCCATCAGC 998

Search completed: December 30, 2005, 03:35:40
Job time : 170 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2005, 02:30:46 ; Search time 808 Seconds
(without alignments)
1944.532 Million cell updates/sec

Title: US-09-990-874B-55
Perfect score: 1046
Sequence: 1 QTIPTGTGYHDGYFYWND.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62
Ygapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xl
-MODE=frame+ p2n.model -DEV=xl
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-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	93.1	596	US-10-307-441-39	Sequence 39, Appl
2	679.5	65.0	818	US-10-425-115-37173	Sequence 37173, A
3	664.5	63.5	705	US-10-213-990-68	Sequence 68, Appl
4	659.5	63.0	850	US-10-425-115-177283	Sequence 177283,
5	648	62.0	739	US-10-213-990-67	Sequence 67, Appl
6	643.5	61.5	588	US-10-237-386-9	Sequence 9, Appl
7	643.5	61.5	678	US-09-803-454-3	Sequence 3, Appl

8	643.5	61.5	983	3	US-09-467-368-1	Sequence 1, Appl
9	638	61.0	942	5	US-10-213-990-71	Sequence 71, Appl
10	627	59.9	1002	5	US-10-213-990-70	Sequence 70, Appl
11	625.5	59.8	666	5	US-10-213-990-65	Sequence 65, Appl
12	625.5	59.8	749	8	US-10-425-115-82922	Sequence 82922, A
13	611.5	58.5	1375	3	US-09-770-621-1	Sequence 1, Appl
14	611.5	58.5	1375	6	US-10-286-993-1	Sequence 1, Appl
15	605.5	57.9	2898	5	US-10-299-393-1	Sequence 1, Appl
16	605.5	57.9	2898	10	US-11-154-793-1	Sequence 64, Appl
17	605	57.8	712	5	US-10-213-990-64	Sequence 8, Appl
18	584.5	55.9	2225	3	US-09-790-070A-8	Sequence 3, Appl
19	554.5	53.0	591	10	US-11-018-645-3	Sequence 17, Appl
20	554.5	53.0	594	10	US-11-018-645-17	Sequence 10, Appl
21	554.5	53.0	628	10	US-11-018-645-10	Sequence 21, Appl
22	554.5	53.0	978	10	US-11-018-645-21	Sequence 5, Appl
23	549	52.5	972	10	US-11-018-645-5	Sequence 5, Appl
24	549	52.5	972	10	US-11-018-645-19	Sequence 19, Appl
25	549	52.5	1009	10	US-11-018-645-11	Sequence 11, Appl
26	502	48.0	555	10	US-11-018-645-1	Sequence 1, Appl
27	502	48.0	561	10	US-11-018-645-13	Sequence 13, Appl
28	502	48.0	598	10	US-11-018-645-9	Sequence 9, Appl
29	502	48.0	8537	10	US-11-018-645-34	Sequence 34, Appl
30	502	48.0	8546	10	US-11-018-645-33	Sequence 33, Appl
31	502	48.0	12763	10	US-11-018-645-35	Sequence 35, Appl
32	501.5	47.9	642	8	US-10-626-583-4	Sequence 4, Appl
33	501.5	47.9	642	9	US-10-626-724-4	Sequence 4, Appl
34	500	47.8	642	8	US-10-626-583-10	Sequence 10, Appl
35	500	47.8	642	8	US-10-626-583-12	Sequence 12, Appl
36	500	47.8	642	9	US-10-626-724-10	Sequence 10, Appl
37	500	47.8	642	9	US-10-626-724-12	Sequence 12, Appl
38	499	47.7	642	8	US-10-626-583-8	Sequence 8, Appl
39	499	47.7	642	9	US-10-626-724-8	Sequence 8, Appl
40	497	47.5	642	8	US-10-626-583-6	Sequence 6, Appl
41	497	47.5	642	9	US-10-626-724-6	Sequence 6, Appl
42	497	47.5	645	6	US-10-237-386-10	Sequence 10, Appl
43	497	47.5	657	6	US-10-237-386-11	Sequence 11, Appl
44	489	46.7	663	3	US-09-909-207-1	Sequence 1, Appl
45	489	46.7	663	3	US-09-909-207-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-307-441-39
; Sequence 39, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and Alkalophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Trx
US-10-307-441-39

Alignment Scores: 8.65e-112 Length: 596
Pred. No.: 974.00 Matches: 179
Score: 96.32% Conservativeness: 4
Percent Similarity: 94.21% Mismatches: 7
Best Local Similarity: 94.21%


```
Query Match: 93.12% Indels: 0
DB: 6 Gaps: 0
US-09-990-874b-55 (1-190) x US-10-307-441-39 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 23 CAACAAATACACACGAAACCGGTTACAAACACGGTTACTTTTACAGCTATTGGAAACGAT 82
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 83 GGCATGGTGGTGTACCTATACAAACCGGCGCGGAGCCAAATTTAGCGTCAATTGGTCT 142
QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 143 AACTCCGGAACCTTCGTAGTGGAAAGGTTGGCAACCCCGGACCAAAATAAGGTGATC 202
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATCTTAAGCGTCTATGGCTGGTCT 262
QY 81 ArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 263 AGAAACCCACTGATTGAATATTACATGTCTGAATTTTCGGTACCTTACAAATCCGATACC 322
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 323 GCGCCACCAAAATTAGCGGAAGTCACCTAGTAGGATCGGTATATGATATCTACCGTACC 382
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 383 CAACGCGTTAATCAGCCATCGATCANTGGAAACCGCCACCTTTTATCAGTACTGGAGTGT 442
QY 141 ArgArgAsnArgSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 443 AGACGTAATCATCGGAGCTCCGGTTCGGTTAATCTGCGAATCATTATGATGATGGCA 502
QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
DB 503 CAGCAAGGTTAAACCTAGTACAATGATTTATCAAAATCGTAGCGTGGAGGCTACTTTC 562
QY 181 SerSerGlySerAlaSerIleThrValSer 190
DB 563 TCGAGTGGTTCGGCTAGTATTACAGTGAGC 592

RESULT 2
US-10-425-115-37173
; Sequence 37173, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 37173
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133906C.1
US-10-425-115-37173

Alignment Scores: 1.05e-74 Length: 818
Pred. No.: 679.50 Matches: 121
Score: 78.42% Conservative: 28
Percent Similarity: 63.68% Mismatches: 40
Best Local Similarity:
```

```
Query Match: 64.96% Indels: 1
DB: 8 Gaps: 1
US-09-990-874b-55 (1-190) x US-10-425-115-37173 (1-818)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 185 CAGACGACCCCAACCGCGGAAGGAACACACACCGCTGCTTCTACTCTTTGGTGGATGTAT 244
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 245 GGTGCTCCAGGTACTTACACCAACGGTGGAGTGGAGCTACAGCGTCACTGGGGA 304
QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 305 AGCGCGGCGCACTTTTGGTGGTAAGGCTGGAACCCCTGGATCGGCC---CGCACCGTT 361
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 362 ACCTACTCGGGCTCTACACACCCCAACCGCAACTCTTACCTTGGCATCTATGGTGGACA 421
QY 81 ArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 422 CGTAACCTCTCTGTCGAATCTATGCTTGGAACTTCGGAACCTATGACCGAGTTCC 481
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 482 CAGGCTAGCAACAGGGTACCGTGAGTCCGACGGCTCTTCTCAAGATCGCTCAGTGG 541
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 542 ACCCTGACTTAACACGCCATCCATCGATCGAACAAGACCTTTTCAGCAGTACTGGTCTGT 601
QY 141 ArgArgAsnArgSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 602 CCGCAGACAGCGCTCCAGCGGATCCGTGAACATGAAGACTCACTTCGATGCTTGGGCC 661
QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
DB 662 AGCAAGGCGCATGACTCTTGGTAGCCACTACTACCAAGATTGTCGCTACCGAGGATCTTC 721
QY 181 SerSerGlySerAlaSerIleThrValSer 190
DB 722 TCCACCGGTTCTGCTCTATCATCTACTGTGAAC 751

RESULT 3
US-10-213-990-68
; Sequence 68, Application US/10213990
; Publication NO. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (705)
US-10-213-990-68

Alignment Scores: 6.46e-73 Length: 705
Pred. No.: 664.50 Matches: 118
Score:
```

Percent Similarity: 76.60% Conservative: 26
Best Local Similarity: 62.77% Mismatches: 39
Query Match: 63.53% Indels: 5
DB: 5 Gaps: 1

US-09-990-874B-55 (1-190) x US-10-213-990-68 (1-705)

```
QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
DB 136 AC GGCTGGAAACAACGGCTACTACTCTCTCGACTGATGGCGCGCGAGTGACC 195
QY 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerHisSerGlyAsnPheVal 46
DB 196 TACACCAATGGCGCGCTGCTACTCGCTCACTGGAGGAACGTGGGCAACTTTGTC 255
QY 47 GlyGlyLysGlyTrpGlnProGlyThrLys-----AsnLysValLysAsn 61
DB 256 GGTGGAAAGGGCTGGAAACCTGGAGCGGTAGGTACCGAGCTTTAAGTAGAACCATCAAC 315
QY 62 PheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
DB 316 TACGGAGGCGAGCTTCAACCCAGCGGCATGGCTACTCTGCTCTACGGCTGGACCAAC 375
QY 82 AsnProLeuLeuGluTyrTrpLeuValGluAsnGlyThrTyrAsnProSerThrGly 101
DB 376 AACCCCTTGAATGAGTACTAGTGTGTGATGCTATGTTACATACAAACCCCGCAGCGGC 435
QY 102 AlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspLeuCysArgThrGln 121
DB 436 GGTACTCTCAGGGGCACTGTCAACACGAGCGGTGGCACTTACACATCTACACGGCCGTT 495
QY 122 ArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArg 141
DB 496 CGCTACATGCTCCCTCCATCGAGGACCAACAGACCTTCAACCGTACTGCTGTGCGGC 555
QY 142 ArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArg 161
DB 556 ACCTCAAGCGTACCGCGCGCACTGTCAACATGGCCCAACCACTTCAACGCTGGAGCAGA 615
QY 162 GlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSer 181
DB 616 CTGGGCATGAACCTGGGAATCACTACACATCCAGATTGTGCCCACTGAGGGTTACCAAGAC 675
QY 182 SerGlySerAlaSerIleThrVal 189
DB 676 AGCGGATCTGCTCCATCACTGTC 699
```

RESULT 4

US-10-425-115-177283
; Sequence 177283, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 177283
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_93271C.1
US-10-425-115-177283

Alignment Scores:
Pred. No.: 3 53e-72 Length: 850
Score: 659.50 Matches: 120

Percent Similarity: 76.17% Conservative: 27
Best Local Similarity: 62.18% Mismatches: 41
Query Match: 63.05% Indels: 5
DB: 8 Gaps: 2

US-09-990-874B-55 (1-190) x US-10-425-115-177283 (1-850)

```
QY 2 ThrIleGlnProGlyThr-----GlyTyrHisAspGlyTyrPheTyrSerTyr 17
DB 210 ACTGCACGGTGGCGGTACCCCGAGCTCCAGGCGCACCCACAACGGCTGCTTACTCTCGG 269
QY 18 TrpAsnAspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGlnPheSerVal 37
DB 270 TGGACCGACGGTGGCGCCCGAGCTACCTACCAACAGAGCGCGCGCAAGTACACGCGTC 339
QY 38 AsnTrpSerAsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsn 57
DB 330 AACTGGAAAGACCGGTGGTAAACATGGTTGGTGAAGGGCTGGAACCTCGTGGCGGCC--- 386
QY 58 LysValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyr 77
DB 387 CGCACCATCACTACTCTCGGTACTACAGCCCGCAGGGTAACTCTTACCTTGGCATCTAC 446
QY 78 GlyTrpSerArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsn 97
DB 447 GGCTGGACCGGCACCCCTTCTCGAGTACTACGTTGTTGAGAACCTTTGGTACTCTACGAC 506
QY 98 ProSerThrGlyValAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIle 117
DB 507 CGGTCTCTCGCGCCAGCGGTCAAGGGCTCCGTCACGACAGCGGCTCGTCTTACAGATT 566
QY 118 CysArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyr 137
DB 567 GCGCAGACTCAGCGTGTCAACCGACCTCCATCGAGCGGCACCAAGACCTTCAACAGTAC 626
QY 138 TrpSerValArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsn 157
DB 627 TGGTCCGTCGCGCAGAACAAAGCGAGCTCCGGCTCCGTCAACATGAAGACCCCACTTCGAC 686
QY 158 AlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGlu 177
DB 687 GGCTGGCGCTCCAAAGGGCATGCGCTCGGTTCAGCACTACCAATCGTGGCCACCGAG 746
QY 178 GlyTyrPheSerSerGlySerAlaSerIleThrValSer 190
DB 747 GGTACTTCTCTCCGGCAGCTCGTCCGATCACCCTTACT 785
```

RESULT 5

US-10-213-990-67
; Sequence 67, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 739
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-67

Alignment Scores:
Pred. No.: 8 04e-71 Length: 739
Score: 648.00 Matches: 118
Percent Similarity: 72.50% Conservative: 27

Best Local Similarity: 59.00%		MisMatches: 38	
Query Match: 61.95%		Indels: 17	
B: 5		Gaps: 1	
S-09-990-874B-55 (1-190) x US-10-213-990-67 (1-739)			
Y	7	ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyGlyValThr	26
b	136	ACCGGCTGGAAACAGCGCTACTACTCTCTGGACTGATGGCGGCGAGCTGACC	195
Y	27	MetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal	46
b	196	TACACCAATGGCGCGGTGGCTCGTACTCGTCACTGGAGGAACGCTGGCAACTTTGTC	255
Y	47	GlyGlyLysGlyTrpGlnProGlyThr	55
b	256	GGTGGAAAGGGCTGGAAACCTCGGAAGCGCTAGTACCGAGCTTTGTCAACGTCGGATGTG	315
Y	56	-----LysAsnLysValIleAsnPheSerGlySerTyrAsnProAsnG1	70
b	316	CAGACTGTGGCTGACAGAAGTAGAACCATCACTACGGAGGCGAGCTTCAACCCGAGCGG	375
Y	70	YAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIleGluTyrTrileVa	90
b	376	CAATGCTACTCGCTGTCTACGGCTGGACCAACCCCTTGATTGAGTACTACGTTGT	435
Y	90	lGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSe	110
b	436	TCAGTCTGATGTTACATACAAACCCGCGAGCGGTACCTTCAGGGCGCACTGTCAACAC	495
Y	110	rAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGluG1	130
b	496	CGAGCGTGGCACTTCAACATCATACACGGCGGTTCGTACATGCTCCCTCCATCGAAGG	555
Y	130	YThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgArgSerSerGlySerVa	150
b	556	CACCAAGACCTTCACCCAGTACTGCTGTGCGCACCTCCCAAGCGTACCGCGGCACTGT	615
Y	150	lAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAs	170
b	616	CACCATGGCCCAACCACTTCAACGCTGGAGCAGACTGGGCATGAACCTGGGAACTCACA	675
Y	170	pTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThrVal	189
b	676	CTACCAAGATTGTGCCACTGAGGGTTACAGAGCGGGATCTGCTTCCATCACTGTC	733
RESULT 6			
S-10-237-386-9			
; Sequence 9, Application US/10237386			
; Publication No. US20030180895A1			
; GENERAL INFORMATION:			
; APPLICANT: Danisco A/S			
; APPLICANT: Sorensen, Jens			
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor			
; FILE REFERENCE: 674509-2046			
; CURRENT APPLICATION NUMBER: US/10/237,386			
; CURRENT FILING DATE: 2002-12-06			
; PRIOR APPLICATION NUMBER: PCT/IB01/00426			
; PRIOR FILING DATE: 2001-03-08			
; PRIOR APPLICATION NUMBER: GB 0005585.5			
; PRIOR FILING DATE: 2000-03-08			
; PRIOR APPLICATION NUMBER: GB 0015751.1			
; PRIOR FILING DATE: 2000-06-27			
; NUMBER OF SEQ ID NOS: 66			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 9			
; LENGTH: 588			
; TYPE: DNA			
; ORGANISM: Thermomyces lanuginosus			
S-10-237-386-9			
Alignment Scores:			
Pred. No.:	2.62e-70	Length:	678

Pred. No.:		Length:	
Score:		Matches:	
Percent Similarity:		Conservative:	
Best Local Similarity:		Mismatches:	
Query Match:		Indels:	
DB:		Gaps:	
US-09-990-874B-55 (1-190) x US-10-237-386-9 (1-588)			
QY	1	GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp	20
DB	4	CAGACAACCCCAACCTCGGAGGCGCTGGCACGATGGTTATTACTATTCTCTGGTGGAGTGAC	63
QY	21	GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer	40
DB	64	GGTGGAGCGCAGCCACCGTACCAACCTGGGAAGCGCGCACCTACGAGATCAGCTGGGA	123
QY	41	AsnSerGlyAsnPheValGlyGlyGlyTrpGlnProGlyThrLysAsnLysValIle	60
DB	124	GATGGCGGTAACTCGTCTGGTGGAAAGGCGCTGGAAACCCCGCGCTGAACCAAGAGCCATC	183
QY	61	AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer	80
DB	184	CACCTTGGAGGGTGTTTACCAGCCAAACGCAACAGCTACTTGGCGTCTACCGTTGGACC	243
QY	81	ArgAsnProLeuIleGluTyrTrileValGluAsnPheGlyThrTyrAsnProSerThr	100
DB	244	CGCAACCCCGCTGGTGGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTCTCTCC	303
QY	101	GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr	120
DB	304	GGTGTCTACGATCTAGAACTGTGAGTGCAGCGTAGCATCTATCGACTTCGCAAGACC	363
QY	121	GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal	140
DB	364	ACTCGCGTCAACGCACTAGCATGCGAGCGGCCAAACCTTCGACCAATACTGTCGTC	423
QY	141	ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla	160
DB	424	CGCCAGGACAGGCGACACGAGCGGTACCGTCCAGACGCGGCTGCCACTTCGACGCTGGCT	483
QY	161	ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr	179
DB	484	CGCGCTGGTTTGAATGTCAACGCTGACCACTACTACGATCGTTGCAACGGAGGGCTAC	543
QY	180	PheSerSerGlySerAlaSerIleThrValSer	190
DB	544	TTACAGACGCGGTATGCTCGCATCACCGTTGCT	576
RESULT 7			
US-09-803-454-3			
; Sequence 3, Application US/09803454			
; Publication No. US20030022280A1			
; GENERAL INFORMATION:			
; APPLICANT: No. US20030022280A1ozymes A/S			
; APPLICANT: Takagi, Shinobu			
; APPLICANT: Terui, Yuri			
; TITLE OF INVENTION: High Expression of Industrial Enzymes			
; FILE REFERENCE: 6125.200-US			
; CURRENT APPLICATION NUMBER: US/09/803,454			
; CURRENT FILING DATE: 2001-03-09			
; NUMBER OF SEQ ID NOS: 52			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 3			
; LENGTH: 678			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Synthetic			
US-09-803-454-3			
Alignment Scores:			
Pred. No.:	2.62e-70	Length:	678

Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 3 Gaps: 1

US-09-990-874B-55 (1-190) x US-09-803-454-3 (1-678)

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QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 94 CAACCACTCCCAATTCGAGGTTGGCATGATGTTATTTATTTCTTGGTGGTCTGAT 153
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 154 CGTGGTGGCTCAAGTACTATTATTAATTTAGAGGTTGGTACCTATGAAATTTCTTGGGCT 213
QY 41 AnSerGlyAsnPheValGlyGlyGlyGlyTrpGlnProGlyThrLysAsnLysValIle 60
DB 214 GATGGTGGTAAATTTAGTTGGTAAAGTTGGAATCCAGGTTTAAATCAAGAGCTATT 273
QY 61 AnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 274 CATTTCGAGGTTTATCAACCAATGTAATCTTATTTAGCTGTTTATGTTGGTACT 333
QY 81 ArgAsnProLeuIleGlyTyrTrpLeuValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 334 AGAATCCATTAGTTGAATATTATATTGTTGAAATTTTGGTACTTATGATCCATCTTCT 393
QY 101 GlyAlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspLysCysArgThr 120
DB 394 GGTGCTACTGATTTAGTACTGTTGAATGCTGATGTTCTTATTATAGATTAGTAAACT 453
QY 121 GlnArgValAsnAlaProSerIleGlyGlyGlyAlaThrPheTyrGlnTyrTrpSerVal 140
DB 454 ACTAGATTAAATGCACCATCTATTGATGACTCAAACTTTCATCAATTTGTTCTGTT 513
QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 514 AGACAAGATAAAGAACTTCTGTAAGTCTGTTCAAACTGGTGTCAATTCGATGCTGGGCT 573
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 574 AGAGCTGGTGTGAATGTTAATGGTGATCAATATTATCAAAATTTGTTCAACTGAAGGTTAT 633
QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
DB 634 TTCTCTTCTGGTTATGCTAGAAATTACTGTTGCT 666
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RESULT 8

US-09-467-368-1
Sequence 1, Application US/09467368
Patent No. US20020160080A1
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
Mullertz, Anette
Knap, Inge Helmer

TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020160080A1o No. US20020160080A1disk of No. US200201600
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,368

FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Thermomyces lanuginosus
STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-467-368-1

Alignment Scores:
Pred. No.: 4,368-70 Length: 983
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 3 Gaps: 1

US-09-990-874B-55 (1-190) x US-09-467-368-1 (1-983)

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QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 124 CAGACNACCCCACTCGAGGGCTGGCAGCATGTTATTACTATCTCTGGTGGAGTGAC 183
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 184 GGTGGAGCGCAGGCCACGTCACCAACCTCGAAGCGCGCACCTACGAGATCAGCTGGGA 243
QY 41 AnSerGlyAsnPheValGlyGlyGlyGlyTrpGlnProGlyThrLysAsnLysValIle 60
DB 244 GATGCGGTAACTCTGCTGGTGGAAAGGGCTGGAAACCCCGCGCTGAACGCAAGAGCCATC 303
QY 61 AnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 304 CACTTTGAGGGTGTTCACGCAACACGCAACACGCTACCTTCGCTTACGGTTGGACC 363
QY 81 ArgAsnProLeuIleGlyTyrTrpLeuValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 364 CGCAACCGCTGGTGGTATTCATCGTCGAGAATTTGGCACCTATGATCTCTCTCC 423
QY 101 GlyAlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspLysCysArgThr 120
DB 424 GGTGTACCGATCTAGGAACTGTCCAGTCGACGCTGATCATCTATCGACTCGCGCAAGACC 483
QY 121 GlnArgValAsnAlaProSerIleGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 484 ACTCGCTCAACGCACTAGCATCGACGCAACCCCAACCTTCGACCAATCTATGCTGGTTC 543
QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 544 CGCCAGGACAAAGCGCACCGCGGTACCGTCCAGACGGGCTGCGACTTCGACGCTGGGCT 603
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 604 CGCGCTGGTGTGAATGTCAACGGTGCACCACTACTACCGAGATCGTTTGCACAGGGGGTAC 663
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DB 574 TCCATCCGCCAAACACAGCGATCCAGCGGCACAGTCACCCACCGCAATCCTTCAAGGCC 633
QY 159 TtpAlaAaGInGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGly 178
DB 634 TGGGCTAGCTGGGGATGAACTGGGTACCCATACTATCAGATTGTTCCACTGAGGGA 693
QY 179 TyrPheSerSerGlySerAlaSerIleThrValSer 190
DB 694 TATGAGACGACGGGTACCTCGACCATCATCTGCTCG 729
RESULT 11
US-10-213-990-65
; Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(666)
US-10-213-990-65
Alignment Scores:
Pred. No.: 4,59e-68 Length: 666
Score: 625.50 Matches: 111
Percent Similarity: 77.11% Conservatives: 31
Best Local Similarity: 60.33% Mismatches: 41
Query Match: 59.80% Indels: 1
DB: 5 Gaps: 1
US-09-990-874B-55 (1-190) x US-10-213-990-65 (1-666)
QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
DB 115 ACTGGCACGAATAACGGCTACTACTCTCTTGGACCGACGGCGCGCCAGGTGACC 174
QY 27 MetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
DB 175 TACACCAACGGCAATGGCGCGCATGATACAGTGCATCGGAACAATCGCGCACTTTGTT 234
QY 47 GlyGlyLeuGlyTrpGlnProGlyThrLysAsnLysValIleAsnPheSerGlySerTyr 66
DB 235 GCTGGAAAGGCTGGAAACCGGCCACGAG--AAAGCGGTACCTACAGCGCTCTCG 291
QY 67 AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIleGlu 86
DB 292 CAGACCCAGGAAACGGCTACCTCTCCGTGTACGGCTGGACGACCACTGCGTGTGCGAA 351
QY 87 TyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGly 106
DB 352 TTCTATCATGTGGAGATTACGCTCTATGACCCCTCCACGGGAGCCACCACTCCGCG 411
QY 107 GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
DB 412 ACCGTGAGAGCGACGGGCCAGTACGTTACCTCTACAGACGACGGCGGACGATGCGCG 471
QY 127 SerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSer 146
DB 472 TCCATCCAGGCGACGGCTACTTTTGACCACTGTTGCGTCTCGGATCTCGGACCGCGCAG 531

QY 147 SerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaAaGInGlyLeuThrLeu 166
DB 532 AGTGGAACTGTGACGACGAGAACCACTTGTATCGTGGAGAAATGCGGGTCTGCATITG 591
QY 167 GlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
DB 592 GGGAACTTGTACTATATGATTTGTTCCGACGAGGGGTACACAGACGAGCGGCTCTGCTACT 651
QY 187 IleThrValSer 190
DB 652 ATCACTGTTTCT 663
RESULT 12
US-10-425-115-82922
; Sequence 82922, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 82922
; LENGTH: 749
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(749)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_175642C.1
US-10-425-115-82922
Alignment Scores:
Pred. No.: 5,39e-68 Length: 749
Score: 625.50 Matches: 113
Percent Similarity: 73.68% Conservatives: 27
Best Local Similarity: 59.47% Mismatches: 49
Query Match: 59.80% Indels: 1
DB: 8 Gaps: 1
US-09-990-874B-55 (1-190) x US-10-425-115-82922 (1-749)
QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 170 CAGAACACCCCCCAACGGCGAGGGTACCCACAACGGCTGCTTCTGGTCTTTGGTGTCTGAT 229
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 230 GCGGTGCGCGCGCTACCTACACCAACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 289
QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 290 AGCGGTGGCAACCTCGTGGTGGAAAGGATGGAAACCCAGGAACTGCC---CGTACCATC 346
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 347 ACCTACTCTGTGTACTTACAACTACAAACGGCAACTCTTACCTTGGCTCTACGGCTGGACC 406
QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 407 CGCAACCCCTTGTGCGAGTACTACGTCGTTGAGAACTTCGCGACCTTACACCCCTCTCC 466
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 467 CAGTCCCAAGAACCAAGGGTACCGCTACCTCTGATGGATCTTCTTCAAGATCGCTCAGTCG 526

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
Db 527 ACCCGTACCAACAGCCCTCCATCGATGCGACGACGACCTTTTCAGCAGTATTGGTCTGTT 586
QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
Db 587 CQTCAAGAACAGCGCTCTTCGCGCTCCGTCATATGAAGACTCACATTGACGCCCTGGGCC 646
QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
Db 647 ACCAAGGCGATGAACCTTGGCCGACGACTACTACCATGATTGGTCCACCGANGTTACTTC 706
QY 181 SerSerGlySerAlaSerIleThrValSer 190
Db 707 TCCACTGGTAAACGGCCAGATCACCGGTCAAC 736

RESULT 13

US-09-770-621-1
; Sequence 1, Application US/09770621
; Patent No. US20010024815A1
; GENERAL INFORMATION:
; APPLICANT: M ntyl, Arja
; APPLICANT: Vehmaanper, Jari
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lahtinen, Tarja
; TITLE OF INVENTION: Production and Secretion of Proteins of
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,621
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/590,563
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332,412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/282,001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 1050.0340003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2500
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

LENGTH: 1375 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: No. US20010024815A1 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 303..1334
US-09-770-621-1
Alignment Scores:
Pred. No.: 7,05e-66 Length: 1375
Score: 611.50 Matches: 108
Percent Similarity: 75.94% Conservative: 34
Best Local Similarity: 57.75% Mismatches: 42
Query Match: 58.46% Indels: 3
Gaps: 3

US-09-990-874b-55 (1-190) x US-09-770-621-1 (1-1375)

QY 4 GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGly 23
Db 447 CAGAACCAACGCGGTACGACACACGGCTACTTCTACTCGTTCTGGACCGCGCCGCG 506
QY 24 GlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGly 43
Db 507 ACCGTCTCCATGACCCCTCCACTCGCGGCGGACGACTACAGCACCTCTGTGGCGGAACACCGGG 566
QY 44 AsnPheValGlyGlyLysGlyTyrPdnProGlyThrLysAsnLysValIleAsnPheSer 63
Db 567 AACTTCGTCCGCGCAAGGGCTGTCCACCGGGGACCG---CGACCGTGACCTTACAC 623
QY 64 GlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnPro 83
Db 624 GCCTCTTCAACCCGTCGGGTAAACGGCTACCTACCGCTCTACGGCTGACCGAGAACCGG 683
QY 84 LeuLeuGlyTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103
Db 684 CTCGTGAGTACTACATCGTCGAGAGCTGGGGCACCTACCGGCCC---ACCGGCACCTAC 740
QY 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123
Db 741 AAG---GGCACCGTCACCCAGCGGGGAAACGTACGACATCTACGAGACCTGGCGGTAC 797
QY 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsn 143
Db 798 AACGGCGGTCTCATCGAGGGCACCGGACCTTCCAGCAGTCTCGGAGCGTCCGCGACGAG 857
QY 144 ArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGly 163
Db 858 AAGCGGACGACGCGCACCATCATCGGCAACCACTTCGACGCTCGCGCCCGCGCCGCGC 917
QY 164 LeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGly 183
Db 918 ATGAACCTGGGCGACGACGACTACCATGATCATGGCGACCGAGGGCTACGAGACGCGGT 977
QY 184 SerAlaSerIleThrValSer 190
Db 978 AGTCCACCGTCTCCATCAGC 998

RESULT 14

US-10-286-993-1
; Sequence 1, Application US/10286993
; Publication No. US20030148453A1
; GENERAL INFORMATION:
; APPLICANT: Mantyla, Arja
; APPLICANT: Paloheimo, Marja
; APPLICANT: Lantto, Raija
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Vehmaanpera, Jari
; TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
; FILE REFERENCE: 1716.0340004
; CURRENT APPLICATION NUMBER: US/10/286,993
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/120,804
; PRIOR FILING DATE: 1998-07-23

Db 1857 GGAACCTTCACCTTCAACCACTACTGGTCAGTTCCGACCGAGAAGCGAGTCGGCGGAACCT 1916
 QY 150 ValAsnThrAlaAsnHisphenAlaTtpAlaAArgGlnGlyLeuThrLeuGlyThrMet 169
 Db 1917 GTCACCAACCGCAACCACTTTCAGCATGGAGGCACTTGGACTTGAATGGGCACTTAT 1976
 QY 170 AspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThrVal 189
 Db 1977 AACTATATGATTGTGTCCACCGAAGGCTACGAGAGCAGTGGCTCTAGTACCATCACAGTG 2036
 QY 190 Ser 190
 Db 2037 TCC 2039

Search completed: December 30, 2005, 05:50:28
 Job time : 823 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2005, 03:32:53 ; Search time 895 Seconds
(without alignments)
111.289 Million cell updates/sec

Title: US-09-990-874B-55
Perfect score: 1046
Sequence: 1 QTIPTGTGYHGDYFYWND.....YQIVAVEGYFGSGSASITVS 190

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4172979 seqs, 262114271 residues

Total number of hits satisfying chosen parameters: 8345958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0990874@cgn_1_1_183 @runat_29122005_095050_5222
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100
-LONGLOG -DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.*
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	643.5	61.5	588	7 US-11-170-653-9	Sequence 9, Appl
2	497	47.5	645	7 US-11-170-653-10	Sequence 10, Appl
3	497	47.5	657	7 US-11-170-653-11	Sequence 11, Appl
4	110	10.5	774	6 US-10-793-626-3243	Sequence 3243, Ap
5	110	10.5	3007	6 US-10-793-626-3846	Sequence 3846, Ap
C 5	110	10.5	3090	6 US-10-793-626-3599	Sequence 3599, Ap
C 7	110	10.5	3864	6 US-10-793-626-3727	Sequence 3727, Ap
8	86.5	8.3	1422	6 US-10-509-464-2	Sequence 2, Appl

9	86	8.2	273	6	US-10-467-657-3589	Sequence 3589, Ap
10	86	8.2	273	6	US-10-467-657-6439	Sequence 6439, Ap
C 11	85.5	8.2	11736	7	US-11-000-463-218	Sequence 218, App
12	83.5	8.0	993	6	US-10-467-657-237	Sequence 237, App
13	83.5	8.0	993	6	US-10-467-657-1113	Sequence 1113, Ap
C 14	82.5	7.9	2403	6	US-10-467-657-2169	Sequence 2169, Ap
15	82.5	7.9	2403	6	US-10-467-657-6469	Sequence 6469, Ap
C 16	80.5	7.7	5682	7	US-11-059-982-2	Sequence 2, Appl
17	80	7.6	2346	6	US-10-416-047-13	Sequence 13, Appl
18	79	7.6	1383	6	US-10-858-730-134	Sequence 134, App
C 19	78.5	7.5	179666	7	US-11-121-086-67	Sequence 67, Appl
20	77.5	7.4	2082	6	US-10-873-528-157	Sequence 197, App
C 21	77	7.4	772	6	US-10-750-185-49101	Sequence 49101, A
22	77	7.4	1404	7	US-11-000-463-663	Sequence 663, App
23	76.5	7.3	1422	6	US-10-509-464-1	Sequence 1, Appl
24	76.5	7.3	1925	6	US-10-909-125-815	Sequence 815, App
C 25	76	7.3	2112	6	US-10-485-517-44	Sequence 44, Appl
C 26	76	7.3	70513	6	US-10-995-561-13368	Sequence 13368, A
C 27	75.5	7.2	1148	6	US-10-793-626-1563	Sequence 1563, Ap
C 28	75.5	7.2	3328	6	US-10-793-626-4195	Sequence 4195, Ap
29	75.5	7.2	116856	7	US-11-143-980-1	Sequence 1, Appl
C 30	75	7.2	95223	7	US-11-117-187-188	Sequence 188, App
C 31	75	7.2	170189	7	US-11-112-908-50	Sequence 50, Appl
32	74.5	7.1	3032	6	US-10-533-355-3	Sequence 3, Appl
33	74	7.1	86081	6	US-10-995-561-13246	Sequence 13246, A
34	73.5	7.0	711	6	US-10-073-301A-8	Sequence 8, Appl
C 35	73.5	7.0	1117	6	US-10-821-234-222	Sequence 222, App
36	73	7.0	1189	6	US-10-750-185-24625	Sequence 24625, A
37	73	7.0	3192	6	US-10-131-826A-75	Sequence 75, Appl
38	73	7.0	65723	6	US-10-995-561-13200	Sequence 13200, A
39	72.5	6.9	702	7	US-11-173-969-9	Sequence 9, Appl
40	72.5	6.9	702	8	US-11-173-320-9	Sequence 9, Appl
41	72.5	6.9	777	6	US-10-512-184-6	Sequence 6, Appl
42	72.5	6.9	777	6	US-10-512-184-8	Sequence 8, Appl
43	72.5	6.9	987	6	US-10-512-184-57	Sequence 57, Appl
44	72.5	6.9	987	6	US-10-512-184-59	Sequence 59, Appl
C 45	72.5	6.9	2996	6	US-10-750-185-53271	Sequence 53271, A

ALIGNMENTS

RESULT 1

US-11-170-653-9
; Sequence 9, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibito
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Thermomyces lanuginosus
US-11-170-653-9

Alignment Scores: 2.21e-66 Length: 588
Pred. No.: 643.50 Matches: 117
Score: 74.87% Conservative: 26

Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 7 Gaps: 1

US-09-990-874B-55 (1-190) x US-11-170-653-9 (1-588)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
DB 4 CAGACAACCCCACTCGGAGGCTGGCAGCATGTTATTACTATTCTCTGGTGGAGTGAC 63

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40
DB 64 GTGGAGCGCAGCCACGTACCAACCTGGAGCGGCACCTTCAGAGATCAGCTGGGA 123

QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 124 GATGGCGGTAACTCTCGTGGTGAAGGCTGGAACCCCGGCTGAACGCAGAGCCATC 183

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLysValValTyrGlyTyrSer 80
DB 184 CACTTTGAGGGTGTATTACCAAGCCCAACGCGCAACAGCTACTTGGCGGTCTACGGTTGGACC 243

QY 81 ArgAsnProLeuIleGlyTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 244 CGCAACCCGCTGGTCGAGTATTACATCGTCGAGAATTTGGCACCTATGATCCTTCCTCC 303

QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 304 GGTGCTACCGATCTAGAACTGTCGAGTGGCGAGGTAGCATCTATCGATCGCAAGACC 363

QY 121 GlnArgValAsnAlaProSerIleGlyThrAlaThrPheTyrGlnTyrTyrSerVal 140
DB 364 ACTCGGCTCAACGCACCTAGCATCGAGCGGCACCCCAACCTTCGACCAATCTGTCGGTC 423

QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAla 160
DB 424 CGCCAGGCAAGCGCACCGGTACCGTCCAGACGGGCTCGCACCTTCGACGCGCTGGCT 483

QY 161 ArgGlnGlyLeuThrLeu--GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 484 CCGCTGGTGTGAATGTCAACGGTGAACCTACTACAGATCTTCCACGGAGGGCTAC 543

QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
DB 544 TTCAGCAGCGGCTATGCTCGCATCACCGTGTCT 576

RESULT 2

US-11-170-653-10
; Sequence 10, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-11-170-653-10

Alignment Scores:
Pred. No.: 5,43e-49 Length: 645
Score: 497.00 Matches: 97
Percent Similarity: 69.78% Conservative: 30
Best Local Similarity: 53.30% Mismatches: 47
Query Match: 47.51% Indels: 8
DB: 7 Gaps: 6

US-09-990-874B-55 (1-190) x US-11-170-653-10 (1-645)

QY 14 PheTyrSerTyrTyrAsnAspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGly 33
DB 100 TACTCGCAAAATGACTGATGGGCGGTATAGTAAACGCTGTCAATGGTCTGGCGGG 159

QY 34 GlnPheSerValAsnTyrSerAsnSerGlyAsnPheValGlyLysGlyTyrGlnPro 53
DB 160 AATTACAGTGTAAATGCTTAATACCGGAATTTTGTGTGTTAAAGTTGGACTACA 219

QY 54 GlyThrLysAsnLysValIleAsnPhe---SerGlySerTyrAsnProAsnGlyAsnSer 72
DB 220 GGTTCGCCATTTAGGACGATAACTATAATGCCGAGTTTGGCGCGCAATGCAATGGA 279

QY 73 TyrLeuAlaValTyrGlyTyrSerArgAsnProLeuIleGlyTyrTyrIleValGluAsn 92
DB 280 TATTTAACTTTATATGTTGGACGAGATCACCTCTCATAGAATATATATGTAGTGATCA 339

QY 93 PheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSerAspGly 112
DB 340 TGGGTACTTATAGACCT---ACTGGACGTATAAA---GGTACTGTAAAGTGTATGGG 393

QY 113 SerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGlyGly---Thr 131
DB 394 GGTACATATGACATATATACAACTACAGCTTATAACGACCTTCCATTTGATGCGCATCGC 453

QY 132 AlaThrPheTyrGlnTyrTyrSerValArgAsnArgSerSerGlySer----- 149
DB 454 ACTACTTTTACCGCATCTGCGAGTGTCCAGTTCGAAGAGACCAACCCGGAAGCAACGCT 513

QY 150 ---ValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGlnGlyLeuThrLeuGlyThr 168
DB 514 ACATACATTTTCAGGCATCATGTGAACGATGGAAGACCATGGAATGATCTGGCGAGT 573

QY 169 ---MetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIle 187
DB 574 AATTGGGCTTACCAAGTCATGCGCAGACAGAGGATATCAAAGTAGTGAAGTCTTAACGTA 633

QY 188 ThrVal 189
DB 634 ACAGTG 639

RESULT 3

US-11-170-653-11
; Sequence 11, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0

1 SEQ ID NO 11
2 LENGTH: 657
3 TYPE: DNA
4 ORGANISM: Unknown
5 FEATURE:
6 OTHER INFORMATION: B. subtilis xylanase sequence with added restriction site
US-11-170-653-11

Alignment Scores:
Pred. No.: 5,578-49 Length: 657
Score: 497.00 Matches: 97
Percent Similarity: 69.78% Conservative: 30
Best Local Similarity: 53.30% Mismatches: 47
Query Match: 47.51% Indels: 8
DB: 6 Gaps: 6

US-09-990-874B-55 (1-190) x US-11-170-653-11 (1-657)

QY 14 PheTyrSerTyrTrpAsnAspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGly 33
DB 106 TACTGGCAAAATGGAGTCTATGGGGCGGTATAGTAACCGCTGTCAATGGGTCTGGCGGG 165
QY 34 GlnPheSerValAsnTrpSerAsnSerGlyAsnPheValGlyGlyTrpGlnPro 53
DB 166 AATTACAGTGTAAATGGTCTAATACCGGAAATTTTGTGTTGTTAAAGTTGGACTACA 225
QY 54 GlyThrLysAsnLysValIleAsnPhe---SerGlySerTyrAsnProAsnGlyAsnSer 72
DB 226 GGTTCGCCCAATTAGGACGATAACTATAATGCGGAGTTTGGCGCGGAAATGGCAATGGA 285
QY 73 TyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIleGluTyrTyrIleValGluAsn 92
DB 286 TATTTAACTTATATGTTGGACGAGATCACTCTCATAGATATATATGTTAGTGATTC 345
QY 93 PheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSerAspGly 112
DB 346 TGGGGTACTTATAGACCT---ACTGAAACGTATAAA---GGTACTGTAAAGTGTATGGG 399
QY 113 SerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGluGly---Thr 131
DB 400 GGTACATATGACATATATACACTACACGTTTATAACGCACCTTCCATTGATGGCGATCGC 459
QY 132 AlaThrPheTyrGlnTyrTrpSerValArgAsnArgSerSerGlySer----- 149
DB 460 ACTACTTTTACGCAGTACGTGGAGTGTTCGCCAGTCGAAGACCAACCGGAGCAACGCT 519
QY 150 ---ValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThr 168
DB 520 ACAATCACTTTCAGCAATCATGTGAACGCATGGAAGAGCCATGGAATGAATCTGGGCACT 579
QY 169 ---MetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIle 187
DB 580 AATTGGGCTTACCAGTCTACGCGCAGACAGGATATCAAAGTAGTGAAGTTCTTAACGTA 639
QY 188 ThrVal 189
DB 640 ACAGTG 645

RESULT 4
US-10-793-626-3243
; Sequence 3243, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793, 626
; CURRENT FILING DATE: 2004-03-04
; PRIOR FILING DATE: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3243

1 LENGTH: 774
2 TYPE: DNA
3 ORGANISM: Artificial Sequence
4 FEATURE:
5 OTHER INFORMATION: Description of Artificial Sequence: synthetic
6 OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3243

Alignment Scores:
Pred. No.: 0,00431 Length: 774
Score: 110.00 Matches: 55
Percent Similarity: 31.36% Conservative: 19
Best Local Similarity: 23.31% Mismatches: 76
Query Match: 10.52% Indels: 86
DB: 6 Gaps: 11

US-09-990-874B-55 (1-190) x US-10-793-626-3243 (1-774)

QY 4 GlnProGlyThrGlyTyr-----HisAspGlyTyrPheTyrSerTyrTrpAsnAspGly 21
DB 85 CAAATAATATGATGGGTACAATCCAAACGACCCCTTATTCATATAGCTAC----- 132
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsn 41
DB 133 -----ACTTACACATCGATCGTGAAGTAACCTACCACCTACTTGG----- 174
QY 42 SerGlyAsnPheValGlyGlyGlyTrpGlnProGlyThrLysAsnLysValIleAsn 61
DB 175 AAAGGTAAAC-----TGGAGTCCAGATCGGTAAATACT----- 207
QY 62 PheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
DB 208 -----TCATATACTAATAATAATACTACAACCTACTATGTTTAC----- 252
QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsn----- 97
DB 253 AATAACTATAGCACTACATAACTACAGTATTAACAACAATTAACAACAATCAATCAATCA 312
QY 98 -----ProSerThrGlyAlaThrLysHisGlyGluVal 108
DB 313 AACACACGCAATCACAAAGAACAACTCAACCGACTGGTGGTTAGGCGCAAGCTATTCA 372
QY 109 ThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIle 128
DB 373 ACATCAAGTAGTAATATGTTTAC-----GTTACAACAACCTTCTCGGCATCATCA 420
QY 129 GluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSerSerGly 148
DB 421 AACGGTGTA-----TCTTTATCAACGCTCGCTCAGCACTCTGCT 459
QY 149 SerVal----- 150
DB 460 AACTTATACACTTCAGGTCAATGATATATTATTTGACAGAGTAGGTGGCAAAATC 519
QY 151 -----AsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThr 165
DB 520 GGTTCACCGTGGGTAAACGCAAAACAACTGGGCAACGCTGCAGCAGCTTCTGTTTACACA 579
QY 166 LeuGlyThrMetAspTyrGln----- 172
DB 580 GTAAACAATTCGCTGCTTAAGGTGCAATCTTACAAACGCTCAAGGTGCATACGACAC 639
QY 173 IleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThr 188
DB 640 GTAGCATCGTTGAAGGTGTAACACGCAATGTTTCAATCAGAGTTTCA 687

RESULT 5
US-10-793-626-3846/c
; Sequence 3846, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; SEQ ID NO 3243

FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3846
LENGTH: 3007
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence

US-10-793-626-3846

Alignment Scores:
Pred. No.: 0.0285 Length: 3007
Score: 110.00 Matches: 55
Percent Similarity: 31.36% Conservative: 19
Best Local Similarity: 23.31% Mismatches: 76
Query Match: 10.52% Indels: 86
DB: 6 Gaps: 11

US-09-990-874B-55 (1-190) x US-10-793-626-3846 (1-3007)

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QY 4 GlnProGlyThrGlyTyr-----HisAspGlyTyrPheTyrSerTyrTrpAsnAspGly 21
DB 2139 CAAAATAATGATGGGTACCAATCCAAACGACCCCTTATCATATAGCTAC-----2092
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsn 41
DB 2091 -----ACTTACACATCGATCGTGAAGGTAACCTACCACCTACTTGG-----2050
QY 42 SerGlyAsnPheValGlyGlyLysGlyTrpGlnProGlyThrLysAsnLysValIleAsn 61
DB 2049 AAAGGTAAC-----TGGAGTCCAGATCGTGTAAATACT-----2017
QY 62 PheSerGlySerTyrAsnProGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
DB 2016 -----TCATATAACTATAATAATTATAACTACACTACTTGTGTAC-----1972
QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsn-----97
DB 1971 AATACTATAGCAACTACATACTACAGTAAATACCAATTTACCAACAACTATCAATCA 1912
QY 98 -----ProSerThrGlyAlaThrLysHisGlyGluVal 108
DB 1911 AACACACGCAATCACAAAGAACAACTCAACCGACTGTGTGGTTAGGCGCAAGCTATTCA 1852
QY 109 ThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIle 128
DB 1851 ACATCAAGTAGTAATGTTTCAC-----GTTTACAACTTCTCGGCATCATCA 1804
QY 129 GluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSerSerGly 148
DB 1803 AACGGTGTA-----TCTTTATCAACGCTCGCTCAGCATCTGTT 1765
QY 149 SerVal-----150
DB 1764 AACTTATACACTTCAGGTCAATGTACATATTATGTTTGCACAGAGTAGGTGGCAAAATC 1705
QY 151 -----AsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThr 165
DB 1704 GGTTCACCGTGGGTAAACGCAAACTCGGCAACGCTGCAGCAGCTTCTGTTTACACA 1645
QY 166 LeuGlyThrMetAspTyrGln-----172
DB 1644 GTAAACAATTCACCTGCTAAAGGTGCAATCTTACAAACGTCACAAAGTGCATACGACAC 1585
QY 173 IleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThr 188
DB 1584 GTAGCATACGTTGAAGGTGTAACAGCAATGTTTCAATCAGAGTTTCA 1537
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RESULT 6

US-10-793-626-3599/c
Sequence 3599, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3599
LENGTH: 3090
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence

US-10-793-626-3599

Alignment Scores:
Pred. No.: 0.0296 Length: 3090
Score: 110.00 Matches: 55
Percent Similarity: 31.36% Conservative: 19
Best Local Similarity: 23.31% Mismatches: 76
Query Match: 10.52% Indels: 86
DB: 6 Gaps: 11

US-09-990-874B-55 (1-190) x US-10-793-626-3599 (1-3090)

```
QY 4 GlnProGlyThrGlyTyr-----HisAspGlyTyrPheTyrSerTyrTrpAsnAspGly 21
DB 2439 CAAAATAATGATGGGTACCAATCCAAACGACCCCTTATCATATAGCTAC-----2392
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsn 41
DB 2391 -----ACTTACACATCGATCGTGAAGGTAACCTACCACCTACTTGG-----2350
QY 42 SerGlyAsnPheValGlyGlyLysGlyTrpGlnProGlyThrLysAsnLysValIleAsn 61
DB 2349 AAAGGTAAC-----TGGAGTCCAGATCGTGTAAATACT-----2317
QY 62 PheSerGlySerTyrAsnProGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
DB 2316 -----TCATATAACTATAATAATTATAACTACAACTACTACTTGTGTAC-----2272
QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsn-----97
DB 2271 AATACTATAGCAACTACATACTACAGTAAATTTACCAACAACTATCAATCAATCA 2212
QY 98 -----ProSerThrGlyAlaThrLysHisGlyGluVal 108
DB 2211 AACACACGCAATCACAAAGAACAACTCAACCGACTGTGTGGTTAGGCGCAAGCTATTCA 2152
QY 109 ThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIle 128
DB 2151 ACATCAAGTAGTAATGTTTCAC-----GTTTACAACTTCTCGGCATCATCA 2104
QY 129 GluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSerSerGly 148
DB 2103 AACGGTGTA-----TCTTTATCAACGCTCGCTCAGCATCTGTT 2065
QY 149 SerVal-----150
DB 2064 AACTTATACACTTCAGGTCAATGTACATATTATGTTTGCACAGAGTAGGTGGCAAAATC 2005
QY 151 -----AsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThr 165
DB 2004 GGTTCACCGTGGGTAAACGCAAACTCGGCAACGCTGCAGCAGCTTCTGTTTACACA 1945
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Db 331 ATACCTGCTTGCAGATGCTCGAAACCTTGGCTGCTACAGGATCATCGAAACCCACCT 390
Qy 98 ProSerThrGlyAlaThrIleHisGlyGluValThrSerAspGlySerValTyrAspIle 117
Db 391 CCTTAACCTGGCACCGATTAACACGTCACAAACCTCACCATCAAACTTGCATCAGTTT 450
Qy 118 CysArgThrGlnArgValAsnAlaProSerIleGlu---GlyThrAlaThrPheTyr--- 135
Db 451 TGTGGAGTCAGAGTTTCAAGTTTCTGGAGTGGAGTCAGGCTATGCTTCTCTGTGGA 510
Qy 136 -----GlnTyrTrp-SerValArg-----AsnArgArgSerSerG1 148
Db 511 AACAACTCTGATTACTGGAAGTACGGAGGAGGAGGAGTACCGAATGCAACAGCGTCTGC 570
Qy 148 ySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyTh 168
Db 571 TTCGGGATCACACCAAC----- 589
Qy 168 rMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleTh 188
Db 590 -----CCTGGTGGCGATG-----GCAGATCATCTCTTTTGC 624
Qy 188 rValSer 190
Db 625 ACTCTCG 631

RESULT 9

US-10-467-657-3589
; Sequence 3589, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3589
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3589

Alignment Scores:
Pred. No.: 0.699 Length: 273
Score: 86.00 Matches: 27
Percent Similarity: 52.05% Conservative: 11
Best Local Similarity: 36.99% Mismatches: 23
Query Match: 8.22% Indels: 12
DB: 6 Gaps: 4

US-09-990-874B-55 (1-190) x US-10-467-657-3589 (1-273)

Qy 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyGlyVal 25
Db 61 GGTAGCGGCTATGGCAACGGCTACGGCAACGGCTACGGCAAC---GGCTACGGCGCGTC 117
Qy 26 ThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPhe 45
Db 118 -----GGCGGGCGGGT-----AGCGGACGGC---TAC 144
Qy 46 ValGlyGlyLeuGlyTrpGlnProGlyThrLysAsnLysValIleAsnPheSerGlySer 65
Db 145 GGCACGGCAACGGCTACAGCAACGGCGGCAACGGCGGACGGCGGCAACGGCGCAAC 204

Qy 66 TyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGly 78
Db 205 GGTAGCGGCAACGGCTATGGCAACGGCTACGGC 243

RESULT 10

US-10-467-657-6439
; Sequence 6439, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6439
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6439

Alignment Scores:
Pred. No.: 0.699 Length: 273
Score: 86.00 Matches: 27
Percent Similarity: 52.05% Conservative: 11
Best Local Similarity: 36.99% Mismatches: 23
Query Match: 8.22% Indels: 12
DB: 6 Gaps: 4

US-09-990-874B-55 (1-190) x US-10-467-657-6439 (1-273)

Qy 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyGlyVal 25
Db 61 GGTAGCGGCTATGGCAACGGCTACGGCAACGGCTACGGCAAC---GGCTACGGCGCGTC 117
Qy 26 ThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPhe 45
Db 118 -----GGCGGGCGGGT-----AGCGGACGGC---TAC 144
Qy 46 ValGlyGlyLeuGlyTrpGlnProGlyThrLysAsnLysValIleAsnPheSerGlySer 65
Db 145 GGCACGGCAACGGCTACAGCAACGGCGGCAACGGCGGACGGCGGCAACGGCGCAAC 204
Qy 66 TyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGly 78
Db 205 GGTAGCGGCAACGGCTATGGCAACGGCTACGGC 243

RESULT 11

US-11-000-463-218/c
; Sequence 218, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463

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; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 218
; LENGTH: 11736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (229)..(11253)
US-11-000-463-218

Alignment Scores:
Pred. No.: 150 Length: 11736
Score: 85.50 Matches: 28
Percent Similarity: 32.77% Conservative: 11
Best Local Similarity: 23.53% Mismatches: 33
Query Match: 8.17% Indels: 47
DB: 7 Gaps: 5

US-09-990-874B-55 (1-190) x US-11-000-463-218 (1-11736)
QY 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrp----- 18
DB 4900 GGCCTCGGGGCTCTTCAAGCACTCGTATAGTGTGGGGTCCCATGGGCGATGTGCT 4841
QY 19 -----AsnAspGlyHisGlyGlyValThr----- 26
DB 4840 CGGCTACCAAGAGAGCTCCATGTGCTCAGGTGGCAGAACTGGTGCAGCTCCACTGAGG 4781
QY 27 ---MetThrLeuGlyProGly-----GlyGlnPheSerValAsnTrpSer 40
DB 4780 CTTGCAGCTGTCAGGCGCGGATGCCAGATGCCCTGCAGAAAGCTCCAGCTCCGGAGGT 4721
QY 41 AsnSerGlyAsnPheValGlyGlyLygLy----- 50
DB 4720 GCTTCTGGGCTCTTTCAGAGTGGCGGGAGGGCGGCGCATGCCATGGGCCATGGAGCGGA 4661
QY 51 -----TrpGlnProGlyThrLysAsnLysValIleAsnPheSerGlySerTyr 66
DB 4660 GGCAGCCCATCTGGCAGCCAGG-----TCCGGCTCTCAC 4625
QY 67 AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIle 85
DB 4624 TCTCCAGCTGTGGTGCCGTTCTTCGAGCCTCTGGCTGGAGCGCAGGTCTCGCCCTG 4568

RESULT 12
US-10-467-657-237
; Sequence 237, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 237
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-237

Alignment Scores:
Pred. No.: 832 Length: 993
Score: 83.50 Matches: 51
Percent Similarity: 33.33% Conservative: 21
Best Local Similarity: 23.61% Mismatches: 71
Query Match: 7.98% Indels: 73
DB: 6 Gaps: 12

US-09-990-874B-55 (1-190) x US-10-467-657-237 (1-993)
QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsn-----App 20
DB 265 TCATCTACGCGCGAGCCCAACCGTCAGCTACTCTCCCGCGATTCAAAATTCGCGAC 324
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 325 CGCAGCAGCAGG-----CAGCGGCTCGCGAGCGCGCATCTTTATCTGTGTCAGC 378
QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlyTrpGlnProGlyThrLysAsnLysValIle 60
DB 379 GACTCC-----GGGGCTACTCTCGTATGCGGAAATTCACCAAGATTATATG 426
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrp 79
DB 427 AAATTCGGGGCGTGGATAGTCTTAACGCGGAAATCGACCTCTTCGCGCGCGCTTCCCC 486
QY 80 ---SerArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnPro 98
DB 487 GTCGCGCAAAACCGCGCTCTCTCGTTC-----TCTACGCGCAGCAGCAGCGCC 534
QY 99 SerThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCys 118
DB 535 GAAACCGCATTTGTCAAAG---GGTAAATCACT----- 564
QY 119 ArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrp 138
DB 565 -----TATCAGGTTTGG 576
QY 139 SerValArg---ArgAsnArgArg-----SerSerGly 148
DB 577 GGCATCCGCGTCCAGAAACGCGCAATTTGTACTTCTTATACGCCCGCGCGGCGGT 636
QY 149 SerValAsn-----ThrAlaAsnHisPhe 156
DB 637 TCTTATATTGGGACACTTCCCAATACCCCGCTCTTTTCTTTATCACGCCCAAT---TTC 693
QY 157 AsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyr----- 171
DB 694 AACCAACACACTGGCAGGCAAAATCTTCGCGACAGCGATTACGGCGCGGATGTGGAT 753
QY 172 ---GlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
DB 754 ATTCAAACGCAACGATTACCGTCCGACCTTTTCGGCGGATGCCACG 801

RESULT 13
US-10-467-657-1113
; Sequence 1113, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia

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Db 624 TTCGCGCGGTATCGGTGAGAAATCTATTTCAAGGATGATCGGTGATGCTTGACGCG 565
QY 166 uGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSe 186
Db 564 AGCGTCGGCAAAATCCGGCGCAGCGCTTCGAGCTGGGTGGCATTCGCTCCGGCGGCATA 505
QY 186 rIleThrValSer 190
Db 504 GCGGCGCGTTTCA 492

RESULT 15

US-10-467-657-6469
; Sequence 6469, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 6469
; LENGTH: 2403
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6469

Alignment Scores:

Pred. No.: 37.4 Length: 2403
Score: 82.50 Matches: 52
Percent Similarity: 34.29% Conservative: 32
Best Local Similarity: 21.22% Mismatches: 97
Query Match: 7.89% Indels: 64
DB: 6 Gaps: 9

US-09-990-874B-55 (1-190) x US-10-467-657-6469 (1-2403)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAsp----- 11
Db 1207 CAGACGCTGGCAACCAAGCGGCTACAAAGACAACTTACGCCATCATGCCCGCCCTT 1266
QY 12 -----GlyTyrPheTyr 15
Db 1267 TCTGCGGATGGCATAAACGAGCGGCGGCAATCGGCGTGTCGCGACAAATTTACC 1326
QY 16 SerTyrTrpAsnAspGly---HisGlyGlyValThrMetThrLeuGlyProGlyGlyGln 34
Db 1327 CGCTTCAGCCACGACGCGGCCCAAGACGCGGACGCGACTGGTGTGTATCCCGGT----- 1380
QY 35 PheSerValAsnTrp-----SerAsnSerGlyAsnPheVal----- 46
Db 1381 -----ATCAAAATGGGATTTACGACACAGCTGGGGCTACGTCGCGCCCAAACTCGGGGTG 1434
QY 47 -----GlyGlyLysGlyTyrGlnPro-----GlyThr 55
Db 1435 CAGGCCACTTATTACAGCTCGACAGTTTCGGCGGGCAAGCATCCCGCAGCGTCGGGCGC 1494
QY 56 LysAsnLysValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAla 75
Db 1495 GTTTTCGCCGTGTCAATATCGACGCGGCGGCAACCTTCGAACGCAATACGCGCTG--- 1551
QY 76 ValTyrGlyTrpSerArganProLeuIleGluTyrTyrIleValGluAsnPhe----- 93
Db 1552 ---TTCGGCGCGGAGTCGTGCAAAACCATCGAGCGCGCCTGTCTACAACTATATTCCT 1608
QY 94 -----GlyThrTyrAsnProSerThrGlyAlaThrLysHisGly 106

Db 1609 GCCAAATCTCAAAACGACCTGCCCAATTTGATTCGTGGAAAGCAGCTTCGGCTACGGG 1668
QY 107 GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
Db 1669 CAGCTTTTCCGGCGAAACCTCTATTACGGC-----AACGACCGCATCAACGCGCC 1719
QY 127 SerIleGluGlyThrAlaThrPheTyrGln-TyrTrpSerValArgArgAsnArgArgSe 146
Db 1720 AACAGCCTTTCCACCGCGGTGCAGAGCCGTATTTTGGACGCGCGCGGAGGAGCGT 1779
QY 146 rSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrIle 166
Db 1780 TTCCCGCGCGGTATCGGTACAGAAATCTATTCAAGGATGATCGGTGATGCTTGACGCG 1839
QY 166 uGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSe 186
Db 1840 AGCGTCGGCAAAATCCCGCAGCGCGTTCCGACTGGGTGGCATTCGCTCCGCGCGGCATA 1899
QY 186 rIleThrValSer 190
Db 1900 GCGCGCGCGTTTCA 1912

Search completed: December 30, 2005, 06:05:33

Job time : 902 secs